

```
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..10
FT /*tag= a
FT /note= "contains phosphorothioate internucleotide
FT linkages"
XX
XX WO9823294-A1.
XX
XX 04-JUN-1998.
XX
XX 26-NOV-1997; 97WO-US022017.
XX
XX 26-NOV-1996; 96US-00757024.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1998-322464/28.
XX
XX Treating respiratory disease with antisense sequences directed against
XX adenosine or bradykinin receptors - with localised delivery to the
XX respiratory system, suitable for long term treatment of asthma, adult
XX respiratory distress syndrome etc.
XX
XX Claim 12; Page 8-24; 47pp; English.
XX
XX Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the
XX human adenosine A1 receptor, the design of which required the secondary
XX structure of this targets mRNA. The adenosine receptor mRNA secondary
XX structure was both analysed and used to construct antisense
XX oligonucleotides containing a phosphorothioate backbone. Once the
XX antisense molecules are created they can be used to target their
XX predetermined target, thus causing the gene product to decrease. The
XX antisense oligonucleotides were targeted to specific mRNA regions
XX containing either a junction between the intron and exon, or where they
XX may overlap the initiation codon. The receptor is a member of the G-
XX protein coupled family of cell surface receptors that have 7-
XX transmembrane segments. These oligonucleotides can be used to treat or
XX prevent conditions associated with bronchoconstriction and/or lung
XX inflammation in humans or other animals e.g. asthma, pulmonary disease,
XX allergy, emphysema and cystic fibrosis
XX
XX Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred.No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GGCGGGC 8
XX |||||
XX Db 3 GGCGGGC 9
XX
XX RESULT 551
XX AAV47410
XX ID AAV47410 standard; DNA; 10 BP.
XX
XX AC AAV47410;
XX
XX 10-NOV-1998 (first entry)
XX
XX Antisense oligonucleotide 910, targeting adenosine A1 receptor.
XX
XX Secondary structure; mRNA; phosphorothioate backbone; G-protein;
XX bronchoconstriction; lung inflammation; asthma; pulmonary disease;
XX allergy; emphysema; cystic fibrosis; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
```

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XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..10
XX FT /*tag= a
XX FT /note= "contains phosphorothioate internucleotide
XX FT linkages"
XX
XX PN WO9823294-A1.
XX
XX PD 04-JUN-1998.
XX
XX PF 26-NOV-1997; 97WO-US022017.
XX
XX PR 26-NOV-1996; 96US-00757024.
XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX
XX PI Nyce JW;
XX
XX DR WPI; 1998-322464/28.
XX
XX Treating respiratory disease with antisense sequences directed against
XX adenosine or bradykinin receptors - with localised delivery to the
XX respiratory system, suitable for long term treatment of asthma, adult
XX respiratory distress syndrome etc.
XX
XX Claim 12; Page 8-24; 47pp; English.
XX
XX Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the
XX human adenosine A1 receptor, the design of which required the secondary
XX structure of this targets mRNA. The adenosine receptor mRNA secondary
XX structure was both analysed and used to construct antisense
XX oligonucleotides containing a phosphorothioate backbone. Once the
XX antisense molecules are created they can be used to target their
XX predetermined target, thus causing the gene product to decrease. The
XX antisense oligonucleotides were targeted to specific mRNA regions
XX containing either a junction between the intron and exon, or where they
XX may overlap the initiation codon. The receptor is a member of the G-
XX protein coupled family of cell surface receptors that have 7-
XX transmembrane segments. These oligonucleotides can be used to treat or
XX prevent conditions associated with bronchoconstriction and/or lung
XX inflammation in humans or other animals e.g. asthma, pulmonary disease,
XX allergy, emphysema and cystic fibrosis
XX
XX Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred.No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GGCGGGC 8
XX |||||
XX Db 1 GGCGGGC 7
XX
XX RESULT 552
XX AAV35934/C
XX ID AAV35934 standard; DNA; 10 BP.
XX
XX AC AAV35934;
XX
XX 26-AUG-1998 (first entry)
XX
XX Primer used in RAPD assay of the invention.
XX
XX Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
XX muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
XX Synthetic.
XX Sus sp.
XX
XX WO9815837-A1.
XX
```

PD 16-APR-1998.
XX
PF 07-OCT-1997; 97WO-GB002741.
XX
PR 07-OCT-1996; 96GB-00020904.
PR 18-FEB-1997; 97GB-00003350.
PR 20-MAR-1997; 97GB-00005796.
PR 09-SEP-1997; 97GB-00019002.
XX
XX (MEAT-) MEAT & LIVESTOCK COMMISSION.
PA
XX Maltin CA, Steven J, Warkup CC;
PI
DR WPI; 1998-240958/21.
XX
PT Assay for alleles or muscle fibre composition characteristic of Duroc
PT type pigs - comprises determination of genotype or muscle fibre
PT properties, used to identify animals for breeding programs and to assess
PT meat quality.
XX
PS Example 3; Page 33; 56pp; English.
XX
CC PCR primers AAV35877-996 were used in a rapid amplification of
CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
CC is used to determine if an animal has an allele for, or muscle fibre
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
CC meat of superior quality (particularly tenderness) but are normally less
CC efficient feed converters and fatter than other types. The assay
CC comprises analysing a tissue sample to determine if the genotype
CC comprises the allele, and genetic features typical of animals with Duroc-
CC type MFC are present. The method is used to select animals that have
CC Duroc characteristics for use in breeding programmes (to develop the
CC animals with Duroc pig characteristics), and to assess meat quality
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCGGCAT 13
Db 9 GCGGCAT 3

RESULT 553
AAx53757
ID AAX53757 standard; DNA; 10 BP.
XX
AC AAX53757;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.

XX 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
PT
XX
PS Disclosure; Page 41; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGGGGC 8
Db 4 GCGGGGC 10

RESULT 554
AAx53778
ID AAX53778 standard; DNA; 10 BP.
XX
AC AAX53778;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.

XX 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
DR New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
PT
XX
XX Disclosure; Page 41; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCGGGC 8
Db 2 GGCGGGC 8

RESULT 555
AAX53768
ID AAX53768 standard; DNA; 10 BP.
XX
AC AAX53768;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.

XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
PI
XX WPI; 1999-229400/19.
DR
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
PT
XX
XX Disclosure; Page 41; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCGGGC 8
Db 3 GGCGGGC 9

RESULT 556
AAX53787
ID AAX53787 standard; DNA; 10 BP.
XX
AC AAX53787;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX

XX WO9913886-A1.
PN
XX
XX 25-MAR-1999.
PD
XX
XX 17-SEP-1998; 98WO-US019419.
PF
XX
XX 17-SEP-1997; 97US-0059160P.
PR
XX 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
XX
PI Nyce JW;
PI WPI; 1999-229400/19.
XX
DR
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 41; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC -end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
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CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 1 GGCGGGC 7

RESULT 557
AAX54553/c
ID AAX54553 standard; DNA; 10 BP.
XX
AC AAX54553;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human adenosine A2b receptor antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.

XX
OS Synthetic.
XX
XX WO9913886-A1.
PN
XX
XX 25-MAR-1999.
PD
XX
XX 17-SEP-1998; 98WO-US019419.
PF
XX
XX 17-SEP-1997; 97US-0059160P.
PR
XX 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
XX
PI Nyce JW;
PI WPI; 1999-229400/19.
XX
DR
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 43; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC -end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
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CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9
Db 9 GCGGGCG 3

RESULT 558
AAZ22665/c
ID AAZ22665 standard; DNA; 10 BP.
XX
AC AAZ22665;
XX
DT 04-JAN-2000 (first entry)
XX
DE T14 primer for amplification of fungal genomic DNA.
XX
KW commercial; assay; test; fungal pathogen; crop protection; cucurbit;
KW primer; PCR; RAPD analysis; isolate; food crop; ss.
XX
OS Synthetic.
XX
PN EP950719-A2.
XX
PD 20-OCT-1999.

XX 10-MAR-1999; 99EP-00104751.
XX 16-MAR-1998; 98US-0078103P.
PR 22-FEB-1999; 99US-00255432.
XX (UYCL-) UNIV CLEMSON.
XX
PI Keinath AP, Somai BM, Dean RA;
XX
DR WPI; 1999-582557/50.
XX
XX Detecting a pathogenic fungus in cucumbers, pumpkins and gourds using
PT recombinant techniques.
XX
PS Example 3; Page 8; 19pp; English.
XX
CC This is a commercial oligonucleotide primer for the PCR-based RAPD
CC analysis of fungal isolates of *Dydimella bryoniae* and *Phoma* species. The
CC new method may be used to distinguish *D. bryoniae* from non-pathogenic
CC *Phoma* species fungal infections in Cucurbits (i.e. cucumbers, pumpkins,
CC watermelons, gourds, cantaloupes, squashes and related plants). The new
CC method of detection of *D. bryoniae* and *Phoma* species infections allows
CC rapid diagnosis even before symptoms are visible as compared to prior art
CC methods which involved growing pure cultures of the pathogens from the
CC infected plants and identifying them under the light microscope. The
CC method leads to the early treatment of the infected plants with
CC fungicides resulting in an increased chance of saving the infected food
CC crops
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGGCAT 13
Db 8 GCGGCAT 2

RESULT 559
AAA33221
ID AAA33221 standard; DNA; 10 BP.
XX
AC AAA33221;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:910.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;

XX WPI; 2000-205971/18.
DR
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Claim 18; Page 379; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
Db 2 GCGGGGC 8

RESULT 560
AAA33230
ID AAA33230 standard; DNA; 10 BP.
XX
AC AAA33230;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:919.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.

XX PR 03-AUG-1998; 98US-0095212P.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI Nyce JW;
XX DR WPI; 2000-205971/18.
XX PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX PS Claim 18; Page 380; 1343pp; English.
XX CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 1 GGCGGGC 7

RESULT 561
AAA33200
ID AAA33200 standard; DNA; 10 BP.
XX
AC AAA33200;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:889.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX OS Homo sapiens.

XX PN WO200009525-A2.
XX PD 24-FEB-2000.
XX PF 03-AUG-1999; 99WO-US017712.
XX PR 03-AUG-1998; 98US-0095212P.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI Nyce JW;
XX DR WPI; 2000-205971/18.
XX PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX PS Claim 18; Page 377; 1343pp; English.
XX CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 4 GGCGGGC 10

RESULT 562
AAA34000/c
ID AAA34000 standard; DNA; 10 BP.
XX
AC AAA34000;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:1689.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
OS WO200009525-A2.
XX 24-FEB-2000.
XX 03-AUG-1999; 99WO-US017712.
XX 03-AUG-1998; 98US-0095212P.
PR (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 474; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
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CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
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CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCGGGCG 9
Db 9 GCGGGCG 3

RESULT 563
AAA33211
ID AAA33211 standard; DNA; 10 BP.
XX
AC AAA33211;
XX
DT 28-JUL-2000 (first entry)
XX

DE Low adenosine antisense oligonucleotide SEQ ID NO:900.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
OS WO200009525-A2.
XX 24-FEB-2000.
XX 03-AUG-1999; 99WO-US017712.
XX 03-AUG-1998; 98US-0095212P.
PR (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Claim 18; Page 378; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
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CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGGGCG 8
Db 3 GCGGGCG 9

RESULT 564
AAA57157

ID AAA57157 standard; DNA; 10 BP.
XX
AC AAA57157;
DT 16-OCT-2000 (first entry)
XX
DE Human intestinal trefoil factor PCR primer restriction site sequence.
XX
KW Human intestinal trefoil factor; hITF; antiulcer; antiinflammatory;
KW antimicrobial; cytostatic; gastrointestinal motility enhancer;
KW peptic ulcer disease; inflammatory bowel disease; anticancer;
KW gastrointestinal tract protection; bacterial infection; radiation injury;
KW neoplastic cancer; ds.
XX
OS Synthetic.
XX
PN US6063755-A.
XX
PD 16-MAY-2000.
XX
PF 07-JUN-1995; 95US-00476705.
XX
PR 14-FEB-1991; 91US-00655965.
PR 13-FEB-1992; 92US-00837192.
PR 25-MAR-1993; 93US-00037741.
PR 02-FEB-1994; 94US-00191352.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Podolsky DK;
XX
DR WPI; 2000-364484/31.
XX
PT New rat intestinal trefoil factor, useful for treating peptic ulcer
PT diseases, or inflammatory bowel diseases and for protecting the
PT intestinal tract from injury caused by bacterial infection, or radiation
PT injury.
XX
PS Disclosure; Col 7; 17pp; English.
XX
CC The present sequence was added to the 5' end of primers used to amplify
CC human intestinal trefoil factor (hITF) cDNA from a human colon cDNA
CC library. The sequence becomes incorporated into the PCR product and, when
CC digested, the sequence will create sticky ends to facilitate cloning of
CC the amplified fragment. hITF may be used for the treatment of peptic
CC ulcers and inflammatory bowel disease, and for protection of the
CC intestinal tract from injury caused by bacterial infection or radiation
CC injury. ITF may also be used to produce monoclonal antibodies for the
CC detection of ITF in an intestinal tissue or blood serum by indirect
CC immunoassay. ITF can also be used to treat neoplastic cancer
XX
SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db |||||
1 GGGCGGC 7

RESULT 565
AAZ77583/c
ID AAZ77583 standard; DNA; 10 BP.
XX
AC AAZ77583;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:11.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;

KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
(GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 63; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen

CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocytic lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGG 7
Db 8 CGGCGGG 2

RESULT 566
AAZ78013/C
ID AAZ78013 standard; DNA; 10 BP.

AC AAZ78013;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:441.

XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089911P.
PR 19-JUN-1998; 98US-0089922P.
PR 19-JUN-1998; 98US-0089933P.
PR 19-JUN-1998; 98US-0089944P.
PR 19-JUN-1998; 98US-0089977P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.

PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.

XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.

XX Claim 1; Page 77; 130pp; English.

XX
CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocytic lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells

XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCGGCAT 13
Db 8 GCGGCAT 2

RESULT 567
AAZ78427/C
ID AAZ78427 standard; DNA; 10 BP.

XX

AC AAZ78427;

XX 10-APR-2000 (first entry)

XX Human dendritic cell SAGE tag, SEQ ID NO:855.

KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
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PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 90; 130pp; English.
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CC with monocytes. Some of the transcripts correspond to known genes or ESTs
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CC cells. Tumour antigen presentation via the MHC (major histocompatibility
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CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
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CC They may be used in vaccines to induce an immune response, particularly

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CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 0 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
Db 10 GGGCGGC 4

RESULT 568
AAZ79040
ID AAZ79040 standard; DNA; 10 BP.
XX
AC AAZ79040;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1468.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.

PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
DR
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
PS Claim 1; Page 107; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9
|||||||
Db 3 GCGGGCG 9

RESULT 569
AAZ79696/c
ID AAZ79696 standard; DNA; 10 BP.
XX
AC AAZ79696;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:2124.

XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
DR
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
PS Claim 1; Page 125; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.

CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGG 7
Db 8 CGGCGGG 2

RESULT 570
AAZ79088/c
ID AAZ79088 standard; DNA; 10 BP.
AC AAZ79088;
XX
DT 10-APR-2000 (first entry)
DE Human dendritic cell SAGE tag, SEQ ID NO:1516.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.

PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 108; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GCGGGCA 12
Db 8 GCGGGCA 2

RESULT 571
AAZ85222
ID AAZ85222 standard; DNA; 10 BP.
XX
AC AAZ85222;
XX
DT 07-APR-2000 (first entry)
XX

DE Metastatic breast tumour cell downregulated transcript tag #4456.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
PI WPI; 2000-106079/09.
XX
DR Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
PT
XX
PS Claim 1; Page 178; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9
Db 1 GCGGGCG 7
|||||
|

RESULT 572
AAZ85111/c
ID AAZ85111 standard; DNA; 10 BP.
XX
AC AAZ85111;
XX

DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4345.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
OS
XX
XX WO9965928-A2.
PN
XX
PD 23-DEC-1999.
XX
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX Roberts BL, Shankara S;
PI WPI; 2000-106079/09.
XX
DR Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
PT
XX
PS Claim 1; Page 175; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGC 8
Db 7 GCGGGC 1
|||||
|

RESULT 573
AAZ81013/c
ID AAZ81013 standard; DNA; 10 BP.
XX

AC	AAZ81013;	
XX		
DT	07-APR-2000 (first entry)	
XX		
DE	Metastatic breast tumour cell upregulated transcript tag #247.	
XX		
KW	Human; metastatic breast tumour tissue; breast cancer; tag; primer;	
KW	non-metastatic breast tumour tissue; gene therapy; anticancer;	
KW	antimetastatic; vaccine; diagnosis; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9965928-A2.	
XX		
PD	23-DEC-1999.	
XX		
PF	18-JUN-1999; 99WO-US013647.	
XX		
PR	19-JUN-1998; 98US-0089853P.	
PR	19-JUN-1998; 98US-0089997P.	
PR	19-JUN-1998; 98US-0090039P.	
PR	19-JUN-1998; 98US-0090040P.	
PR	19-JUN-1998; 98US-0090041P.	
XX		
PA	(GENZ) GENZYME CORP.	
PA	(ROBE/) ROBERTS B L.	
PA	(SHAN/) SHANKARA S.	
XX		
PI	Roberts BL, Shankara S;	
XX		
DR	WPI; 2000-106079/09.	
XX		
PT	Isolated polynucleotides differentially expressed between metastatic and	
PT	non-metastatic breast cancer cells, useful for diagnosis, prevention and	
PT	treatment of cancer.	
XX		
PS	Claim 1; Page 64; 219pp; English.	
XX		
CC	AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts	
CC	that are preferentially transcribed in the metastatic breast tumour	
CC	tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942	
CC	to AAZ86677 represent tags corresponding to distinct transcripts that are	
CC	preferentially transcribed in the primary or non-metastatic breast tumour	
CC	tissue (i.e. are downregulated in metastatic breast tumour cells). These	
CC	transcripts can be used for diagnosis, prognosis, monitoring and	
CC	treatment of breast cancer, particularly where metastatic. Diagnosis is	
CC	by standard immunoassays or hybridisation/amplification reactions.	
CC	Compounds that modulate expression of the transcripts are potentially	
CC	useful for treatment of (metastatic) breast cancer, while promoters from	
CC	the transcripts are used to direct expression, in selected cell types, of	
CC	e.g. therapeutic genes (also ribozymes or antisense sequences),	
CC	particularly an antigen-encoding sequence for use in gene or cell-based	
CC	vaccines. Polypeptides encoded by the transcripts are also useful in	
CC	vaccines; for diagnosing breast cancer and for raising specific	
CC	antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic	
CC	agents. Host cells that produce the polypeptides can be used to expand	
CC	and isolate populations of educated, antigen-specific immune effector	
CC	cells, e.g. cytotoxic T lymphocytes, and these used for adoptive	
CC	immunotherapy	
XX		
SQ	Sequence 10 BP; 0 A; 7 C; 2 G; 1 T; 0 U; 0 Other;	
Query Match 43.8%; Score 7; DB 1; Length 10;		
Best Local Similarity 100.0%; Pred. No.3.4e+02;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	5 GGGCGGC 11	
Db	10 GGGCGGC 4	
RESULT 574		
AAZ82036		

ID	AAZ82036 standard; DNA; 10 BP.	
XX		
AC	AAZ82036;	
XX		
DT	07-APR-2000 (first entry)	
XX		
DE	Metastatic breast tumour cell upregulated transcript tag #1270.	
XX		
KW	Human; metastatic breast tumour tissue; breast cancer; tag; primer;	
KW	non-metastatic breast tumour tissue; gene therapy; anticancer;	
KW	antimetastatic; vaccine; diagnosis; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9965928-A2.	
XX		
PD	23-DEC-1999.	
XX		
PF	18-JUN-1999; 99WO-US013647.	
XX		
PR	19-JUN-1998; 98US-0089853P.	
PR	19-JUN-1998; 98US-0089997P.	
PR	19-JUN-1998; 98US-0090039P.	
PR	19-JUN-1998; 98US-0090040P.	
PR	19-JUN-1998; 98US-0090041P.	
XX		
PA	(GENZ) GENZYME CORP.	
PA	(ROBE/) ROBERTS B L.	
PA	(SHAN/) SHANKARA S.	
XX		
PI	Roberts BL, Shankara S;	
XX		
DR	WPI; 2000-106079/09.	
XX		
PT	Isolated polynucleotides differentially expressed between metastatic and	
PT	non-metastatic breast cancer cells, useful for diagnosis, prevention and	
PT	treatment of cancer.	
XX		
PS	Claim 1; Page 92; 219pp; English.	
XX		
CC	AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts	
CC	that are preferentially transcribed in the metastatic breast tumour	
CC	tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942	
CC	to AAZ86677 represent tags corresponding to distinct transcripts that are	
CC	preferentially transcribed in the primary or non-metastatic breast tumour	
CC	tissue (i.e. are downregulated in metastatic breast tumour cells). These	
CC	transcripts can be used for diagnosis, prognosis, monitoring and	
CC	treatment of breast cancer, particularly where metastatic. Diagnosis is	
CC	by standard immunoassays or hybridisation/amplification reactions.	
CC	Compounds that modulate expression of the transcripts are potentially	
CC	useful for treatment of (metastatic) breast cancer, while promoters from	
CC	the transcripts are used to direct expression, in selected cell types, of	
CC	e.g. therapeutic genes (also ribozymes or antisense sequences),	
CC	particularly an antigen-encoding sequence for use in gene or cell-based	
CC	vaccines. Polypeptides encoded by the transcripts are also useful in	
CC	vaccines; for diagnosing breast cancer and for raising specific	
CC	antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic	
CC	agents. Host cells that produce the polypeptides can be used to expand	
CC	and isolate populations of educated, antigen-specific immune effector	
CC	cells, e.g. cytotoxic T lymphocytes, and these used for adoptive	
CC	immunotherapy	
XX		
SQ	Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;	
Query Match 43.8%; Score 7; DB 1; Length 10;		
Best Local Similarity 100.0%; Pred. No.3.4e+02;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	6 GGCGGCA 12	
Db	3 GGCGGCA 9	
Query Match 43.8%; Score 7; DB 1; Length 10;		
Best Local Similarity 100.0%; Pred. No.3.4e+02;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	6 GGCGGCA 12	
Db	3 GGCGGCA 9	

RESULT 575
AAZ82118
ID AAZ82118 standard; DNA; 10 BP.
XX
AC AAZ82118;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1352.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 95; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoded sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCGGGCG 9
| | | | |
Db 4 GCGGGCG 10

RESULT 576
AAZ82210
ID AAZ82210 standard; DNA; 10 BP.
XX
AC AAZ82210;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1444.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 97; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
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CC the transcripts are used to direct expression, in selected cell types, of
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CC particularly an antigen-encoded sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCGGGCG 9

Db 3 GCGGGCG 9
RESULT 577
AAZ81107/c
ID AAZ81107 standard; DNA; 10 BP.
XX
AC AAZ81107;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #341.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 67; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
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CC treatment of breast cancer, particularly where metastatic. Diagnosis is
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CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GCGGGCA 12
|||||
Db 9 GCGGGCA 3
RESULT 578
AAZ81674/c
ID AAZ81674 standard; DNA; 10 BP.
XX
AC AAZ81674;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #908.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 82; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 7 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||||||
Db 9 GGGCGGC 3

RESULT 579
AAZ83948/c
ID AAZ83948 standard; DNA; 10 BP.

XX AAZ83948;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #3182.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Claim 1; Page 144; 219pp; English.

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy

SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7
|||||||
Db 8 CGGCGGG 2

RESULT 580
AAZ82637/c
ID AAZ82637 standard; DNA; 10 BP.

XX AAZ82637;

XX 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #1871.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

XX 19-JUN-1998; 98US-0090039P.

XX 19-JUN-1998; 98US-0090040P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Claim 1; Page 109; 219pp; English.

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy

XX
SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCGGC 11
| | | | | | |
Db 7 GGGCGGC 1
RESULT 581
AAZ84974/c
ID AAZ84974 standard; DNA; 10 BP.
XX
AC AAZ84974;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4208.
XX
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 171; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
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CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CGGCATC 14
| | | | | | |
Db 10 CGGCATC 4
RESULT 582
AAZ85908
ID AAZ85908 standard; DNA; 10 BP.
XX
AC AAZ85908;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5142.
XX
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 195; 219pp; English.
XX
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CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX

SQ Sequence 10 BP; 0 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGCGGGC 8
Db |||||
4 GGCGGGC 10

RESULT 583
AAZ86394
ID AAZ86394 standard; DNA; 10 BP.
XX
AC AAZ86394;
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5628.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 207; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
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CC particularly an antigen-encoded sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in

CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX

SQ Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GCGGGCA 12
Db 2 GCGGGCA 8
|||||

RESULT 584
AAA93863/c
ID AAA93863 standard; DNA; 10 BP.
XX
AC AAA93863;
XX
DT 11-JAN-2001 (first entry)
XX
DE Oligonucleotide used in computational methodology SEQ ID 31.
XX
KW Biopolymer; sequence cluster; sequence analysis; ss.
XX
OS Synthetic.
XX
PN US6109776-A.
XX
PD 29-AUG-2000.
XX
PF 21-APR-1998; 98US-00063450.
XX
PR 21-APR-1998; 98US-00063450.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Haas J;
XX
DR WPI; 2000-586307/55.
XX
PT Computational method and system for identifying clusters of sequences
PT within a set of sequences, useful for identifying, e.g. DNA-binding
PT sites.
XX
PS Disclosure; Col 35; 38pp; English.
XX

A computational analysis method can be used to identify new biopolymer
CC sequence clusters from sequence sets. The method comprises placing each
CC sequence into a new cluster, and calculating an initial information
CC weight matrix. Other sequences from the set are added to the cluster and
CC the information weight matrix of the cluster is re-computed until the
CC information content of the matrix falls below a threshold. The method is
CC useful for identifying potential DNA-binding sites from a set of
CC oligonucleotide sequences. The method and system may also be used to
CC analyse different types of sequences, e.g. the sequences of amino acid
CC subunits in protein polymers may be analysed to identify common or
CC conserved amino acid subunit sub-sequences within the polymers that
CC correspond to common structural features within a family of proteins. The
CC present sequence represents a synthetic oligonucleotide used to
CC illustrate the method of the invention
XX

SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

QY 10 GCATCGT 16
Db 9 GCATCGT 3

RESULT 585
AAC74190
ID AAC74190 standard; cDNA; 10 BP.
XX
AC AAC74190;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human monocyte and dendritic cell expressed gene oligonucleotide #277.
XX
KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW autoimmune disease; tumour; ss.
XX
OS Homo sapiens.
XX
PN WO200060074-A1.
XX
PD 12-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-JP002019.
XX
PR 01-APR-1999; 99JP-00095481.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-619172/59.
XX
PT Groups of genes expressed in human dendritic cells at a greater or lesser extent than in monocytes for investigation and diagnosis of autoimmune disease and tumors.
XX
PS Claim 19; Page 16; 95pp; Japanese.
XX
CC The present invention describes a group of genes consisting of 100 genes which are highly expressed in human dendritic cells; a group of genes which are expressed at a higher frequency in human dendritic cells than in human monocytes; and a group of genes which are expressed at lower frequency in human dendritic cells than in human monocytes. Each group of genes are characterised in that cDNAs of these genes respectively have the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114 to AAC74213), each is continuous with the base sequence 5'-CATG-3', located most closely to the poly-A region. The sequences can be used for the investigation of the role and mechanism of the involvement of dendritic cells in the immune system and for the study and diagnosis of diseases in which dendritic cells play a significant role, e.g. cancers and autoimmune diseases
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9
Db 3 GCGGGCG 9

RESULT 586
AAZ90635
ID AAZ90635 standard; DNA; 10 BP.
XX
AC AAZ90635;
XX
DT 13-JUN-2000 (first entry)

XX Human adipose tissue gene related primer.
DE
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
KW
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Disclosure; Page 39; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAZ90634-636) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90634-36 represent PCR primers related to the human adipose tissue genes
XX
SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCATCGT 16
Db 1 GCATCGT 7

RESULT 587
AAA56550
ID AAA56550 standard; DNA; 10 BP.
XX
AC AAA56550;
XX
DT 07-SEP-2000 (first entry)
XX
DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:444.
XX
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag; granulocyte-macrophage colony-stimulating factor; characterisation; GM-CSF; identification; diagnosis; gene specificity; oncogenesis; disease onset mechanism; genetic disease; drug development; ss.
XX
OS Homo sapiens.
XX
PN WO200024892-A1.
XX
PD 04-MAY-2000.
XX
PF 28-OCT-1999; 99WO-JP005982.
XX
PR 28-OCT-1998; 98JP-00307532.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-350734/30.

XX Genes most frequently expressed in human monocytes and GM-macrophages and
PT M-macrophages studied and with cDNAs characterized, for study of gene
PT specificity, disease onset mechanism, drug development and diagnosis.
XX
PS Claim 43; Page 128; 138pp; Japanese.
XX
CC The present invention describes 100 human genes, which are expressed most
CC frequently in human monocytes. The cDNA of each gene has a sequence fully
CC defined in the specification, and lacking the CATG sequence located
CC adjacent to polyA region. Also described are: (1) an antibody
CC specifically for the protein encoded by any of the genes; (2)
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC which are expressed most frequently in human macrophages, differentiated
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC the cDNA of each gene has a fully defined sequence, given in the
CC specification, lacking the base sequence CATG located most closely to the
CC poly A region; (4) an antibody specifically for the protein encoded by
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC sequences of (3). The genes and cDNAs, are used for the study of gene
CC specificity and disease onset mechanism e.g. oncogenesis, genetic
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC specifically claimed oligonucleotide tag sequences for human genes
CC expressed in monocytes and macrophages
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9
Db |||||
3 GCGGGCG 9

RESULT 588
AAA03580
ID AAA03580 standard; DNA; 10 BP.
XX
AC AAA03580;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:864.
XX
KW Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
KW adenosine A2a receptor; adenosine Ab receptor; adenosine A3 receptor;
KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
KW endotoxin release; ARDS; acute respiratory distress syndrome;
KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
KW supraventricular tachycardia; allergic rhinitis; acute inflammation;
KW chronic obstructive pulmonary disease; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9963938-A2.
XX
PD 16-DEC-1999.
XX
PF 08-JUN-1999; 99WO-US012775.
XX
PR 08-JUN-1998; 98US-0088501P.
PR 09-JUN-1998; 98US-00093972.
PR 09-JUN-1998; 98US-0088657P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Hill JL;
XX
DR WPI; 2000-116433/10.
XX

PT Novel composition for treating or preventing e.g. cardiopulmonary and
PT renal injury.
XX
PS Claim 17; Page 36; 252pp; English.
XX
CC The present invention describes a pharmaceutical composition, comprising
CC at least one agent (I) that prevents, alleviates and/or inhibits
CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
CC (Ib), containing less than 15% adenosine (A), that is antisense to target
CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3',
CC ends or segments between coding and non-coding sequences), or to all
CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and
CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
CC and (Ib), and optionally also contains one or more surfactants. The
CC compositions are used to prevent, alleviate and/or treat adenosine
CC receptor-mediated cardiac, lung and/or renal damage or failure
CC (particularly where associated with ischaemia, toxin release and/or
CC administration of drugs or imaging agents, e.g. adenosine for treating
CC supraventricular tachycardia); (adult) respiratory distress syndrome
CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
CC pulmonary disease; cardiopulmonary hypoxia associated with administration
CC of stress-test agents, particularly where such conditions are associated
CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to
CC AAA03715 represent specifically claimed phosphorothioate antisense
CC oligonucleotides for use in the composition of the present invention.
CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other
CC phosphorothioate oligonucleotides used in the exemplification of the
CC present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGCG 8
Db |||||
2 GCGGGCG 8

RESULT 589
AAA03589
ID AAA03589 standard; DNA; 10 BP.
XX
AC AAA03589;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:873.
XX
KW Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
KW adenosine A2a receptor; adenosine Ab receptor; adenosine A3 receptor;
KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
KW endotoxin release; ARDS; acute respiratory distress syndrome;
KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
KW supraventricular tachycardia; allergic rhinitis; acute inflammation;
KW chronic obstructive pulmonary disease; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9963938-A2.
XX
PD 16-DEC-1999.
XX
PF 08-JUN-1999; 99WO-US012775.
XX
PR 08-JUN-1998; 98US-0088501P.
PR 09-JUN-1998; 98US-00093972.
PR 09-JUN-1998; 98US-0088657P.
XX

PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Hill JL;
XX
XX WPI; 2000-116433/10.
DR
XX
PT Novel composition for treating or preventing e.g. cardiopulmonary and
PT renal injury.
XX
XX Claim 17; Page 36; 252pp; English.
XX
CC The present invention describes a pharmaceutical composition, comprising
CC at least one agent (I) that prevents, alleviates and/or inhibits
CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
CC (Ib), containing less than 15% adenosine (A), that is antisense to target
CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3',
CC ends or segments between coding and non-coding sequences), or to all
CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and
CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
CC and (Ib), and optionally also contains one or more surfactants. The
CC compositions are used to prevent, alleviate and/or treat adenosine
CC receptor-mediated cardiac, lung and/or renal damage or failure
CC (particularly where associated with ischaemia, toxin release and/or
CC administration of drugs or imaging agents, e.g. adenosine for treating
CC supraventricular tachycardia); (adult) respiratory distress syndrome
CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
CC pulmonary disease; cardiopulmonary hypoxia associated with administration
CC of stress-test agents, particularly where such conditions are associated
CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to
CC AAA03715 represent specifically claimed phosphorothioate antisense
CC oligonucleotides for use in the composition of the present invention.
CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other
CC phosphorothioate oligonucleotides used in the exemplification of the
CC present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 1 GGCGGGC 7

RESULT 590
AAA03559
ID AAA03559 standard; DNA; 10 BP.
XX
AC AAA03559;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:843.
XX
KW Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
KW adenosine A2a receptor; adenosine Ab receptor; adenosine A3 receptor;
KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
KW endotoxin release; ARDS; acute respiratory distress syndrome;
KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
KW supraventricular tachycardia; allergic rhinitis; acute inflammation;
KW chronic obstructive pulmonary disease; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9963938-A2.
XX
PD 16-DEC-1999.
XX

PF 08-JUN-1999; 99WO-US012775.
XX
PR 08-JUN-1998; 98US-0088501P.
PR 09-JUN-1998; 98US-00093972.
PR 09-JUN-1998; 98US-0088657P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Hill JL;
XX
DR WPI; 2000-116433/10.
XX
PT Novel composition for treating or preventing e.g. cardiopulmonary and
PT renal injury.
XX
XX Claim 17; Page 36; 252pp; English.
XX
CC The present invention describes a pharmaceutical composition, comprising
CC at least one agent (I) that prevents, alleviates and/or inhibits
CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
CC (Ib), containing less than 15% adenosine (A), that is antisense to target
CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3',
CC ends or segments between coding and non-coding sequences), or to all
CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and
CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
CC and (Ib), and optionally also contains one or more surfactants. The
CC compositions are used to prevent, alleviate and/or treat adenosine
CC receptor-mediated cardiac, lung and/or renal damage or failure
CC (particularly where associated with ischaemia, toxin release and/or
CC administration of drugs or imaging agents, e.g. adenosine for treating
CC supraventricular tachycardia); (adult) respiratory distress syndrome
CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
CC pulmonary disease; cardiopulmonary hypoxia associated with administration
CC of stress-test agents, particularly where such conditions are associated
CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to
CC AAA03715 represent specifically claimed phosphorothioate antisense
CC oligonucleotides for use in the composition of the present invention.
CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other
CC phosphorothioate oligonucleotides used in the exemplification of the
CC present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 4 GGCGGGC 10

RESULT 591
AAA03570
ID AAA03570 standard; DNA; 10 BP.
XX
AC AAA03570;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:854.
XX
KW Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
KW adenosine A2a receptor; adenosine Ab receptor; adenosine A3 receptor;
KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
KW endotoxin release; ARDS; acute respiratory distress syndrome;
KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
KW supraventricular tachycardia; allergic rhinitis; acute inflammation;
KW chronic obstructive pulmonary disease; ss.
XX
OS Homo sapiens.

OS Synthetic.
PN WO9963938-A2.
XX
PD 16-DEC-1999.
XX
PF 08-JUN-1999; 99WO-US012775.
XX
PR 08-JUN-1998; 98US-0088501P.
PR 09-JUN-1998; 98US-00093972.
PR 09-JUN-1998; 98US-0088657P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Hill JL;
XX
DR WPI; 2000-116433/10.
XX
PT Novel composition for treating or preventing e.g. cardiopulmonary and
PT renal injury.
XX
PS Claim 17; Page 36; 252pp; English.
XX
CC The present invention describes a pharmaceutical composition, comprising
CC at least one agent (I) that prevents, alleviates and/or inhibits
CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
CC (Ib), containing less than 15% adenosine (A), that is antisense to target
CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3',
CC ends or segments between coding and non-coding sequences), or to all
CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and
CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
CC and (Ib), and optionally also contains one or more surfactants. The
CC compositions are used to prevent, alleviate and/or treat adenosine
CC receptor-mediated cardiac, lung and/or renal damage or failure
CC (particularly where associated with ischaemia, toxin release and/or
CC administration of drugs or imaging agents, e.g. adenosine for treating
CC supraventricular tachycardia); (adult) respiratory distress syndrome
CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
CC pulmonary disease; cardiopulmonary hypoxia associated with administration
CC of stress-test agents, particularly where such conditions are associated
CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to
CC AAA03715 represent specifically claimed phosphorothioate antisense
CC oligonucleotides for use in the composition of the present invention.
CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other
CC phosphorothioate oligonucleotides used in the exemplification of the
CC present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db |||||
3 GGCGGGC 9

RESULT 592
AAF19333
ID AAF19333 standard; DNA; 10 BP.
XX
AC AAF19333;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human adenosine A1 receptor polynucleotide fragment #900.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 120; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db |||||
3 GGCGGGC 9

RESULT 593

AAAF19343
ID AAF19343 standard; DNA; 10 BP.
XX
AC AAF19343;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human adenosine A1 receptor polynucleotide fragment #910.
KW
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 120; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX

SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
 |||||||
Db 2 GCGGGGC 8

RESULT 594
AAAF19352
ID AAF19352 standard; DNA; 10 BP.
XX
AC AAF19352;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human adenosine A1 receptor polynucleotide fragment #919.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 120; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX

CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
Db 1 GCGGGGC 7

RESULT 595
AAF20122/c
ID AAF20122 standard; DNA; 10 BP.
XX
AC AAF20122;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human adenosine A2b receptor polynucleotide fragment #1689.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 124; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the

CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system peptide
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGGC 9
Db 9 GCGGGGC 3

RESULT 596
AAF19322
ID AAF19322 standard; DNA; 10 BP.
XX
AC AAF19322;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human adenosine A1 receptor polynucleotide fragment #889.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX

PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 119; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCGGGC 8
Db 4 GGCGGGC 10

RESULT 597
AAA47487
ID AAA47487 standard; DNA; 10 BP.
XX
AC AAA47487;
XX
DT 20-OCT-2000 (first entry)
XX
DE NotI adapter sequence.

XX TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;
KW graft versus-host diseases; rheumatoid arthritis; psoriasis;
KW inflammatory bowel disease; septic shock; ulcerative colitis;
KW Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
KW Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia;
KW autoimmune disease; myasthenia gravis; autoimmune diabetes;
KW systemic lupus erythematosus; transgenic animal; diagnosis; prognosis;
KW prophylactic; therapeutic; ss.

XX Synthetic.
OS
XX WO200039284-A1.
PN
XX
PD 06-JUL-2000.
XX

PF 23-DEC-1999; 99WO-US031025.

XX
PR 30-DEC-1998; 98US-00223546.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
PI Holtzman DA;
XX
XX WPI; 2000-465743/40.
DR
XX
XX Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224
PT and 239 polypeptides useful for the treatment of asthma, rheumatoid
PT arthritis, psoriasis and autoimmune diseases.
PT
XX
PS Disclosure; Page 20; 209pp; English.
XX
CC Nucleic acids encoding TANGO polypeptides are useful as modulating agents
CC for regulating cellular processes like asthma, graft versus-host
CC diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease,
CC septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous
CC leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,
CC Lyme's disease, cachexia and autoimmune diseases e.g. myasthenia gravis,
CC autoimmune diabetes and systemic lupus erythematosus. The nucleic acids
CC are also useful for producing transgenic animals and the TANGO
CC polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239
CC sequences are useful in forensic biology, for diagnostic assays,
CC prognostic assays, pharmacogenomics and for monitoring clinical trials.
CC TANGO polypeptides are suitable for both prophylactic and therapeutic
CC methods for treating a subject at risk of a disorder or having a disorder
CC associated with aberrant TANGO expression. A wide range of cellular
CC disorders can be treated
XX
SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGCGGCG 11
Db 1 GGCGGCG 7

RESULT 598
ABN80674/C
ID ABN80674 standard; DNA; 10 BP.

XX
AC ABN80674;

XX
DT 15-JUL-2002 (first entry)

XX
DE Universal high frequency bacterial PCR primer #5.

XX
KW Primer; probe; affinity purification; cloning; biosynthetic pathway;
KW hybridization screening; restriction endonuclease; universal; PCR; ss.

XX
OS Synthetic.

XX
PN WO200112861-A1.

XX
PD 22-FEB-2001.

XX
PF 18-AUG-2000; 2000WO-US022743.

XX
PR 19-AUG-1999; 99US-0149788P.

PR 19-SEP-1999; 99US-0149822P.

XX
PA (OMNI-) OMNISCIENCE PHARM.

XX
PI Fomenkov A, Huang Y, Chaparian MG, Zheng S;

XX
DR WPI; 2001-211237/21.

PT New primers and probes useful for targeted cloning and enrichment of

PT genes and gene clusters for affinity purification of genes or in cloning
XX associated biosynthetic pathway genes.

PS Disclosure; Page 26; 74pp; English.

XX The invention relates to a set of novel primers and probes. The genes
CC cloned are used in affinity purification of genes, and for cloning
CC associated biosynthetic pathway genes. The gene probes/primers may be
CC used in the discovery and characterization of bioactive compound coding
CC sequences and gene clusters, as well as in the discovery of either single
CC genes or entire clusters of adjacent genes involved in the total
CC synthesis of compounds of interest, e.g. secondary metabolite
CC biosynthetic pathways the products of which comprise very useful
CC libraries for antibiotic and other therapeutic compound screening. The
CC cloned genes are further useful for hybridization screening. The sequence
CC represents a universal high frequency bacterial CDS decamer PCR primer
XX

SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||
Db 10 GGGCGGC 4

RESULT 599
ABN80673/c
ID ABN80673 standard; DNA; 10 BP.

XX

AC ABN80673;

XX 15-JUL-2002 (first entry)

DE Universal high frequency bacterial PCR primer #4.

XX Primer; probe; affinity purification; cloning; biosynthetic pathway;
KW hybridization screening; restriction endonuclease; universal; PCR; ss.

XX Synthetic.

XX WO200112861-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US022743.

XX 19-AUG-1999; 99US-0149788P.

XX 19-SEP-1999; 99US-0149822P.

XX (OMNI-) OMNISCIENCE PHARM.

XX Fomenkov A, Huang Y, Chaparian MG, Zheng S;

XX WPI; 2001-211237/21.

XX New primers and probes useful for targeted cloning and enrichment of
PT genes and gene clusters for affinity purification of genes or in cloning
PT associated biosynthetic pathway genes.

PS Disclosure; Page 26; 74pp; English.

XX The invention relates to a set of novel primers and probes. The genes
CC cloned are used in affinity purification of genes, and for cloning
CC associated biosynthetic pathway genes. The gene probes/primers may be
CC used in the discovery and characterization of bioactive compound coding
CC sequences and gene clusters, as well as in the discovery of either single
CC genes or entire clusters of adjacent genes involved in the total
CC synthesis of compounds of interest, e.g. secondary metabolite
CC biosynthetic pathways the products of which comprise very useful
CC libraries for antibiotic and other therapeutic compound screening. The

CC cloned genes are further useful for hybridization screening. The sequence
CC represents a universal high frequency bacterial CDS decamer PCR primer
XX
SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||
Db 10 GGGCGGC 4

RESULT 600
AAF90454

ID AAF90454 standard; DNA; 10 BP.

XX

AC AAF90454;

XX 06-AUG-2001 (first entry)

DE Egr-1 binding site.

XX Promoter; Egr-1; transcription factor; human; vulnery; wound healing;
KW dermatological; antiulcer; ds.

XX Mammalia.

XX WO200140460-A1.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-EP011997.

XX 01-DEC-1999; 99GB-00028430.

XX (GLAX) GLAXO GROUP LTD.

XX Braddock M, Campbell CJ;

XX WPI; 2001-374827/39.

XX Screening modulators of epidermal growth factor receptor-1 useful for
PT wound healing, involves providing expression system that is regulated by
PT Egr-1 and analyzing effect of compound on expression from system.

PS Disclosure; Page 5; 81pp; English.

XX The present sequence is that of an Egr-1 binding site that has the
CC capability of conferring Egr-1 dependency upon a promoter. An Egr-1
CC binding site in found within the promoter (see AAF90451) of the human Egr
CC -1 gene, and may be involved in autoregulation. Transcription factor Egr-
CC 1 is a potential regulator of over 30 genes and plays a role in growth,
CC development and differentiation. It is induced upon injury to the
CC vascular endothelium. The Egr-1 promoter, its variants, or any other
CC promoter that is regulatable by Egr-1, can be used in an expression
CC system to screen for compounds capable of modulating Egr-1 expression.
CC Such compounds are used as medicaments or in drug development programs,
CC particularly in the identification of drugs for wound healing (claimed).
CC Conditions that may be treated include dermal ulcers arising from
CC ischaemia and neuropathy associated with diabetes, deep vein thrombosis,
CC post-operative scarring associated with e.g. cataracts, skin graft
CC procedures, burns, psoriasis, and tissue engineering. Identified
CC compounds may also be useful to reduce scarring during wound healing,
CC restenosis following percutaneous trans-luminal coronary angioplasty, to
CC modulate vessel wall calcification, treat cancer or other cell
CC proliferative disorders, inhibit fibrotic conditions, for e.g. pulmonary
CC and liver fibrosis, and to prevent alopecia

XX Sequence 10 BP; 0 A; 2 C; 7 G; 0 T; 0 U; 1 Other;

SQ Sequence 10 BP; 0 A; 2 C; 7 G; 0 T; 0 U; 1 Other;

Query Match

43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 77.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGCGGC 11
|||:| |||
Db 1 GCGKGGGC 9

RESULT 601
AAH64280/c
ID AAH64280 standard; cDNA; 10 BP.
XX
AC AAH64280;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1120.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
|||||||
Db 7 GGGCGGC 1

RESULT 602
AAH64083
ID AAH64083 standard; cDNA; 10 BP.
XX
AC AAH64083;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 923.
XX

KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 13; Page 60; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGGGGC 8
|||||||
Db 3 GCGGGGC 9

RESULT 603
AAH64084
ID AAH64084 standard; cDNA; 10 BP.
XX
AC AAH64084;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 924.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX Claim 13; Page 60; 94pp; English.
PS
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 3 GGCGGGC 9

RESULT 604
AAH64098/c
ID AAH64098 standard; cDNA; 10 BP.
XX
AC AAH64098;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 938.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
OS
XX WO200138577-A2.
PN
XX 31-MAY-2001.
PD
XX 21-NOV-2000; 2000WO-US031922.
PF
XX 24-NOV-1999; 99US-00448480.
PR
XX (UYJO) UNIV JOHNS HOPKINS.
PA
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
DR
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 13; Page 60; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 0 A; 7 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCGGC 11
Db 9 GGCGGC 3

RESULT 605
AAH63527/c
ID AAH63527 standard; cDNA; 10 BP.
XX
AC AAH63527;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 367.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
OS
XX WO200138577-A2.
PN
XX 31-MAY-2001.
PD
XX 21-NOV-2000; 2000WO-US031922.
PF
XX 24-NOV-1999; 99US-00448480.
PR
XX (UYJO) UNIV JOHNS HOPKINS.
PA
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
DR
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 13; Page 47; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
Db 10 CGGCATC 4

RESULT 606
AAH63544/c
ID AAH63544 standard; cDNA; 10 BP.
XX
AC AAH63544;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 384.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
KW Homo sapiens.
XX WO200138577-A2.
PN 31-MAY-2001.
XX 21-NOV-2000; 2000WO-US031922.
PF 24-NOV-1999; 99US-00448480.
XX (UYJO) UNIV JOHNS HOPKINS.
PA Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
DR New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
PT Claim 13; Page 47; 94pp; English.
PS The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db |||||||
7 GGCGGGC 1

RESULT 607
AAD20712
ID AAD20712 standard; DNA; 10 BP.
XX
AC AAD20712;
XX
DT 03-JAN-2002 (first entry)
XX
DE Primer #4 used to detect human GPIBA gene polymorphism.
XX
KW Human; haplotyping; glycoprotein Ib (platelet) alpha protein; GPIBA;
KW Bernard-Soulier syndrome; platelet-type von Willebrand disease; HIV;
KW Alzheimer's disease; polymorphism; human immunodeficiency virus; primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200175065-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010671.
XX
PR 03-APR-2000; 2000US-0194341P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX

PI Bentivegna SC, Choi JY, Kliem SE, Koshy B, Parks KE;
XX WPI; 2001-626427/72.
DR
XX
PT New haplotypes of the glycoprotein Ib platelet alpha polypeptide gene are
PT useful for diagnosis and drug discovery for treating Bernard Soulier
PT syndrome, platelet-type von Willebrand disease, HIV and Alzheimer's
PT disease.
XX
PS Claim 18; Page 14; 66pp; English.
XX
CC The invention relates to methods for haplotyping glycoprotein Ib
CC (platelet) alpha polypeptide (GPIBA) gene of an individual. The method
CC involves determining if the individual has one of the GPIBA haplotypes or
CC haplotype pairs. The methods of the invention are useful for disease
CC diagnosis and in the discovery and development of drugs for treating
CC diseases associated with GPIBA activity e.g. Bernard-Soulier syndrome,
CC platelet-type von Willebrand disease, HIV and Alzheimer's disease. The
CC present sequence is a primer used for detecting human GPIBA gene
CC polymorphisms
XX
SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db |||||||
4 GGCGGGC 10

RESULT 608
AAH32888/c
ID AAH32888 standard; cDNA; 10 BP.
XX
AC AAH32888;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ:261.
XX
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-304369/32.
XX
PT LPS activated human monocyte expression gene group.
XX
PS Claim 19; Page 43; 52pp; Japanese.
XX
CC The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC CATG-3', nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role. AAH32628
CC to AAH32943 represent specifically claimed LPS activated human monocyte
CC expression gene cDNA tags from the present invention. AAH32944 represents

CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCGGGC 8
Db 7 GGCGGGC 1

RESULT 609
AAH32889
ID AAH32889 standard; cDNA; 10 BP.
XX
AC AAH32889;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ:262.
XX
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-304369/32.
XX
LPS activated human monocyte expression gene group.
PT
XX
PS Claim 19; Page 43; 52pp; Japanese.
XX
CC The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role. AAH32628
CC to AAH32943 represent specifically claimed LPS activated human monocyte
CC expression gene cDNA tags from the present invention. AAH32944 represents
CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCGGCG 9
Db 3 GGCGGCG 9

RESULT 610
AAF34183/c
ID AAF34183 standard; DNA; 10 BP.
XX

AC AAF34183;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:922.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 32; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCGGCA 12
Db 8 GGCGGCA 2

RESULT 611

AAF42380/c
ID AAF42380 standard; DNA; 10 BP.
XX
AC AAF42380;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9119.
XX
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 325; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCATCGT 16
| | | | | | | |
Db 10 GCATCGT 4

RESULT 612
AAF34736
ID AAF34736 standard; DNA; 10 BP.
XX
AC AAF34736;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1475.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 52; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCATCGT 16
Db 1 GCATCGT 7

RESULT 613
AAF33729/C
ID AAF33729 standard; DNA; 10 BP.
XX AAF33729;
AC AAF33729;
XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:468.
DE XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX WO200077214-A2.
PN XX
XX 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 392; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
Db 7 CGGCATC 1

RESULT 614
AAF35209/c
ID AAF35209 standard; DNA; 10 BP.
XX
AC AAF35209;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1948.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 69; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX

SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCGGCAT 13
Db 10 GCGGCAT 4
RESULT 615
AAF37089/c
ID AAF37089 standard; DNA; 10 BP.
XX
AC AAF37089;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3828.
XX
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 136; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GCATCGT 16
Db 7 GCATCGT 1
RESULT 616
AAF41929/c
ID AAF41929 standard; DNA; 10 BP.
XX
AC AAF41929;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8668.
XX
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 309; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.

CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCATCGT 16
Db 8 GCATCGT 2

RESULT 617
AAAF43170/c
ID AAF43170 standard; DNA; 10 BP.
XX
AC AAF43170;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11309.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
DR
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 353; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 5 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
Db 7 GGCGGCA 1

RESULT 618
AAAF40066/c
ID AAF40066 standard; DNA; 10 BP.
XX
AC AAF40066;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6805.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
DR
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 243; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX
SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||||||
Db 10 GGGCGGC 4

RESULT 619
AAF34402/c
ID AAF34402 standard; DNA; 10 BP.

XX AAF34402;

XX 23-MAR-2001 (first entry)

DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1141.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS
XX WO200077214-A2.

PN
XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

PA Velculescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 40; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention

XX
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
|||||||
Db 7 CGGCATC 1

RESULT 620
AAF39330/c
ID AAF39330 standard; DNA; 10 BP.

XX AAF39330;

XX 23-MAR-2001 (first entry)

DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6069.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS
XX WO200077214-A2.

PN
XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

PA Velculescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

XX Example; Page 216; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCATCGT 16
Db |||||
7 GCATCGT 1

RESULT 621
AAF40942/c
ID AAF40942 standard; DNA; 10 BP.
XX
AC AAF40942;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7681.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
DR
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 274; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGG 7
Db |||||
7 CGCGCGG 1

RESULT 622
AAS99952
ID AAS99952 standard; DNA; 10 BP.
XX
AC AAS99952;
XX
DT 12-MAR-2002 (first entry)
XX
DE Even-skipped homeobox 1 (EVX1) gene allele-specific oligonucleotide #29.
XX
KW Even-skipped homeo box 1; EVX1; neurological disease; drug screening;
KW haplotyping; single nucleotide polymorphism; SNP; human; ss;
KW allele-specific oligonucleotide.
XX
OS Homo sapiens.
XX
PN WO200190120-A2.
XX
PD 29-NOV-2001.
XX
PF 21-MAY-2001; 2001WO-US016559.
XX
PR 19-MAY-2000; 2000US-0205437P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Duda A, Kliem SE, Kumar AM;
XX WPI; 2002-089913/12.
DR
XX
PT Novel genetic variants of even-skipped homeo box 1, EVX1 gene useful for
PT therapeutic purposes and for expressing EVX1 protein useful in
PT identifying drugs to treat neurological diseases.
XX
PS Claim 18; Page 13; 69pp; English.
XX
CC The invention relates to an isolated polynucleotide (I), comprising a
CC nucleotide sequence which is a polymorphic variant of a reference
CC sequence for the even-skipped homeo box 1 (homologue of Drosophila)
CC (EVX1) gene or its fragment, or a polymorphic variant of a reference
CC sequence for a EVX1 cDNA or its fragment. EVX1 polypeptide (II) is useful

CC for screening for drugs targeting the polypeptide, by contacting the EVX1
CC polymorphic variant with a candidate agent and assaying for binding
CC activity. A method is described for identifying an association between a
CC trait such as a clinical response to a drug targeting EVX1 and a
CC haplotype or haplotype pair of EVX1 gene. The methods are useful in
CC developing diagnostic tests and therapeutic treatments for neurological
CC diseases. (I) is useful for studying the expression and function of EVX1
CC and expressing EVX1 protein for use in screening for candidate drugs to
CC treat diseases related to EVX1 activity. The polymorphism and haplotype
CC data are useful for validating whether EVX1 is a suitable target for
CC drugs to treat neurological diseases, screening for such drugs and
CC reducing bias in clinical trials of such drugs. (I) is useful for
CC therapeutic purposes. (I) is useful for determining if an individual has
CC one of the haplotypes 1-4 or the haplotype pairs. Establishing the EVX1
CC haplotype or haplotype pair of an individual is useful for improving the
CC efficiency and reliability of several steps in the discovery and
CC development of drugs for treating diseases associated with EVX1 activity
CC e.g. neurological diseases. The haplotyping method is useful to validate
CC EVX1 as a candidate target for treating a specific condition or disease
CC predicted to be associated with EVX1 activity. (I) is useful for studying
CC expression of the EVX1 isogenes in vivo, for in vivo screening and
CC testing of drugs against EVX1 protein and for testing the efficacy of
CC therapeutic agents and compounds for neurological diseases in a
CC biological system. Antibody raised against (II) is useful for diagnostic
CC and prognostic formats and therapeutic methods, for immunoprecipitating
CC (II) from solution, for detecting EVX1 protein isoforms in biological
CC samples, frozen tissue sections, cells which have been fixed or unfixed
CC and prepared on slides, for use in immunocytochemical,
CC immunohistochemical and immunofluorescence techniques. AAS99924-AAS99958
CC represent human EVX1 gene allele-specific oligonucleotides of the
CC invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9
| | | | |
Db 1 GCGGGCG 7

RESULT 623
ABLS2168/c
ID ABL52168 standard; DNA; 10 BP.
XX
AC ABL52168;
XX
DT 12-JUL-2002 (first entry)
XX
DE Human PER1 preferred oligonucleotide primer SEQ ID NO:93.
XX
KW Human; period (Drosophila) homolog 1; PER1; polymorphic variant;
KW polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200222650-A2.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028780.
XX
PR 13-SEP-2000; 2000US-0232468P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Duda A, Kliem SE, Koshy B;
XX
DR WPI; 2002-393941/42.
XX

PT Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT for therapeutic purposes, for studying the expression and function of the
PT polynucleotide, and for expressing the homolog.
XX
PS Claim 19; Page 15; 162pp; English.
XX
CC The present invention describes an isolated human period (Drosophila)
CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
CC or its fragment, or a polymorphic variant of a reference sequence
CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also
CC describes methods for genotyping and haplotyping the PER1 gene of an
CC individual. (I) is useful in studying the expression and function of
CC PER1, and in expressing PER1 protein for use in screening for candidate
CC drugs to treat diseases related to PER1 activity. (I) is useful for
CC therapeutic purposes. A recombinant non-human organism transformed or
CC transfected with (I) can be used for studying expression of the PER1
CC isogenes in vivo, for in vivo screening and testing of drugs targeted
CC against PER1 protein, and for testing the efficacy of therapeutic agents
CC and compounds for disorders associated with circadian rhythm regulation.
CC The present sequence represents a preferred oligonucleotide primer for
CC human PER1, which is used in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CCGGGCG 10
| | | | |
Db 9 CCGGGCG 3

RESULT 624
ABK95853
ID ABK95853 standard; DNA; 10 BP.
XX

AC ABK95853;
XX
DT 24-SEP-2002 (first entry)
XX

DE Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #24.
XX
KW Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
KW glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
KW amino acid transporter disorder; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO200244198-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US044781.
XX
PR 30-NOV-2000; 2000US-0250254P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Kazemi A, Russo DP, Sausker EA;
XX
DR WPI; 2002-519580/55.
XX
PT Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency and
PT reliability in drug development for treating cancers.
XX
PS Claim 17; Page 16; 139pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC first nucleotide sequence which comprises solute carrier family 1
CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes

CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
CC which is a polymorphic variant of a reference sequence for SLC1A4
CC protein. Also described are methods for: (1) haplotyping or genotyping
CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
CC gene of an individual; (3) identifying an association between a trait and
CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) is useful
CC in screening for drugs targeting (III) that are useful for treating
CC cancer, neurological diseases and amino acid transporter disorders. The
CC methods are useful for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with SLC1A4 activity. The haplotyping method is also
CC used by the pharmaceutical research scientist to validate SLC1A4 as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
CC and amino acid transporter disorders, and in the design of clinical
CC trials for treating a specific condition of disease associated with
CC SLC1A4 activity. The methods are also useful for screening compounds
CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4
CC gene allele-specific oligonucleotides, primer extension oligonucleotides
CC and related PCR primers used to identify single nucleotide polymorphisms
CC (SNP) of the gene

SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCATCG 15

Db 2 GGCATCG 8

RESULT 625

ABK96067
ID ABK96067 standard; DNA; 10 BP.

XX AC ABK96067;

XX AC ABK96067;

DT 24-SEP-2002 (first entry)

XX Human LIPE gene polymorphism detection oligonucleotide primer #42.
DE Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;
KW polymorphism; primer; ss.

XX Homo sapiens.

XX WO200240502-A2.

PN 23-MAY-2002.

XX 16-NOV-2001; 2001WO-US043518.

XX 16-NOV-2000; 2000US-0249302P.

XX (GENA-) GENAISSANCE PHARM INC.

PI Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;

XX WPI; 2002-519369/55.

XX Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT diseases associated with LIPE activity, e.g. obesity and male sterility.

XX Claim 17; Page 16; 142pp; English.

XX The present invention relates to a new polynucleotide comprising a
CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)
CC isogenes. The invention is useful in screening for drugs targeting LIPE
CC isogenes that are useful for treating obesity and male sterility. The

CC methods of the invention are useful for improving the efficiency and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with LIPE activity. The polynucleotide
CC is useful in studying the expression and function of LIPE, and in
CC expressing LIPE protein for use in screening for candidate drugs to treat
CC diseases related to LIPE activity. It is also useful in studying the
CC effect of the variation on the biological activity of LIPE as well as on
CC the binding affinity of candidate drugs targeting LIPE for the treatment
CC of obesity and male sterility. The invention is useful for studying the
CC expression of LIPE isogenes in vivo, for in vivo screening and testing of
CC drugs targeted against LIPE protein, and for testing the efficacy of
CC therapeutic agents and compounds for treating obesity and male sterility
CC in a biological system. The present nucleic acid sequence represents one
CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
CC used in the invention to detect polymorphisms in the human LIPE gene

SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12

Db 3 GGCGGCA 9

RESULT 626

AAS96206/C
ID AAS96206 standard; DNA; 10 BP.

XX AC AAS96206;

XX 26-FEB-2002 (first entry)

DE Human Acetylcholinesterase gene ASO primer extension primer #24.

XX Human; ss; PCR primer; allele specific oligonucleotide; ASO; ACHE;
KW acetylcholinesterase; polymorphic variant; haplotyping; genotyping;
KW neurological disease; Parkinson's disease; Alzheimer's disease; cancer;
KW leukaemia; tumour; chromosome 7q22; primer extension.

XX Homo sapiens.

XX WO200179219-A2.

XX 25-OCT-2001.

XX 11-APR-2001; 2001WO-US011853.

XX 14-APR-2000; 2000US-0197173P.

XX (GENA-) GENAISSANCE PHARM INC.
XX (KAZE/) KAZEMI A.

PI Bentivegna SC, Chew A, Choi JY, Koshy B;

XX WPI; 2002-055248/07.

XX New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
PT useful in expressing ACHE protein for use in screening for candidate
PT drugs to treat diseases related to ACHE activity, e.g. neurological
PT diseases or cancer.

XX Claim 18; Page 14; 79pp; English.

XX The invention relates to a polynucleotide comprising a polymorphic
CC variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
CC complement, the variant comprising an ACHE isogene defined by a haplotype
CC selected from haplotypes 1-20 listed in the specification. Also included
CC are methods for haplotyping and genotyping the ACHE gene of an
CC individual, a method for predicting a haplotype pair for the ACHE gene of
CC an individual, a method for identifying an association between a trait

CC and at least one haplotype or haplotype pair of ACHE gene, recombinant
CC nonhuman organisms transformed or transfected with the polynucleotide
CC where the organism expresses ACHE protein encoded by the first nucleotide
CC sequence or encoded by the polymorphic variant sequence, an isolated
CC antibody specific for and immunoreactive with ACHE, a method of screening
CC for drugs targeting the polypeptide contacting ACHE, a polymorphic variant
CC with a candidate agent and assaying for binding activity, a computer
CC system for storing and analysing polymorphism data for ACHE gene and a
CC genome anthology for ACHE gene which comprises ACHE isogenes defined by
CC haplotypes 1-20 given in the specification. The Polymorphisms are useful
CC for studying the biological function of ACHE as well as in identifying
CC drugs targeting this protein for the treatment of disorder related to its
CC abnormal expression or function. The polymorphic variants may also be
CC used in screening for compounds targeting ACHE to treat a specific
CC condition or disease predicted to be associated with ACHE activity e.g.
CC neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
CC cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
CC 7q22. The present sequence is the allele specific (ASO) portion of a PCR
CC primer used in a primer extension experiment to detect the polymorphic
CC ACHE variants of the invention
XX

SQ Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7
|||||||
Db 8 CGGCGGG 2

RESULT 627
ABK81360
ID ABK81360 standard; DNA; 10 BP.
XX
AC ABK81360;

XX
DT 13-AUG-2002 (first entry)
XX
DE Human FOS gene allele-specific oligonucleotide PCR primer #3.
XX

KW Human; v-fos FBJ murine osteosarcoma viral oncogene homologue; FOS; PCR;
KW cytostatic; gene therapy; single nucleotide polymorphism; haplotyping;
KW haplotype pair; developmental bone disorder; cancer; tumour; ss; primer;
KW chromosome 14q21-q31.
XX

OS Homo sapiens.
XX
PN WO200232931-A2.
XX
PD 25-APR-2002.
XX
PF 19-OCT-2001; 2001WO-US046142.
XX
PR 19-OCT-2000; 2000US-0241620P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX

PI Anastasio AE, Kliem SE, Koshy B, Lee HH;
XX
DR WPI; 2002-435529/46.
XX

PT Novel genetic variants of V-Fos FBJ Murine Osteosarcoma Viral Oncogene
PT Homolog (FOS) isogenes, useful for improving efficiency and reliability
PT in drug development for treating developmental bone disorders.
XX

PS Claim 17; Page 14; 73pp; English.
(X)

CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding the human v-fos FBJ murine osteosarcoma viral oncogene homologue
CC (FOS) polypeptide. A method for haplotyping the FOS gene in an individual
CC comprises identifying the nucleotide at one or more polymorphic sites and

CC determining whether one of the copies of the gene is defined by one of
CC the FOS haplotypes given in the specification or whether both copies are
CC defined by a haplotype pair. This method is useful in genotyping, whereby
CC all possible haplotype pairs can be assigned to specific genotypes. An
CC association between a trait and a haplotype or haplotype pair of the FOS
CC gene can be identified by comparing the frequency of the haplotype or
CC haplotype pair in a population exhibiting the trait with the frequency of
CC the haplotype or haplotype pair in a reference population, where a higher
CC haplotype frequency in the trait population indicates the trait is
CC associated with the haplotype or haplotype pair. FOS and its
CC corresponding DNA are used for studying the expression and function of
CC FOS, for use in screening for candidate drugs to treat diseases related
CC to FOS activity, such as developmental bone disorders and tumours. The
CC sequences are also useful for studying the effect of variation on the
CC biological activity of FOS as well as on the binding affinity of
CC candidate drugs targeting FOS. Sequences ABK81358-ABK81377 represent
CC allele-specific oligonucleotide PCR primers used for detecting FOS gene
XX polymorphisms

SQ Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGCGGG 10
|||||||
Db 4 CGGCGGG 10

RESULT 628
ABQ71649
ID ABQ71649 standard; DNA; 10 BP.
XX

AC ABQ71649;

XX
DT 28-AUG-2002 (first entry)

XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:1641.

XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

OS Homo sapiens.
OS Synthetic.

XX
PN WO200242459-A2.

XX
PD 30-MAY-2002.

XX
PF 20-NOV-2001; 2001WO-US043438.

XX
PR 20-NOV-2000; 2000US-00716637.

XX
PA (SANG-) SANGAMO BIOSCIENCES INC.

XX
PI Liu Q;

XX
DR WPI; 2002-500284/53.

XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX

PS Example 1; Page 51; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it

CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
Db 3 GGCGGCA 9

RESULT 629
ABQ71648
ID ABQ71648 standard; DNA; 10 BP.

AC ABQ71648;

XX 28-AUG-2002 (first entry)

DE Zinc finger protein related oligonucleotide target SEQ ID NO:1640.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

OS Homo sapiens.
OS Synthetic.

XX WO200242459-A2.

PN 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX

PS Example 1; Page 51; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is

CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX

SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
Db 3 GGCGGCA 9

RESULT 630
ABA98376
ID ABA98376 standard; DNA; 10 BP.

XX ABA98376;

XX 30-JUL-2002 (first entry)

DE SCN2B gene polymorphisms oligonucleotide primer #2.

XX Human; sodium channel voltage gated type 2 beta polypeptide; ds;

KW gene therapy; neuroprotective; demyelinating disease.

XX Homo sapiens.

XX WO200179547-A1.

XX 25-OCT-2001.

XX 03-APR-2001; 2001WO-US010743.

XX 13-APR-2000; 2000US-0196597P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Choi JY, Koshy B;

XX WPI; 2002-075072/10.

XX New polynucleotide containing polymorphisms in the human sodium channel
PT voltage gated type 2 beta polypeptide (SCN2B) gene, for developing drugs
PT for treating demyelinating diseases.

XX Claim 17; Page 13; 63pp; English.

XX This invention relates to an isolated polynucleotide which is a
CC polymorphic variant of a reference sequence for sodium channel voltage
CC gated type 2 beta polypeptide (SCN2B) gene. The methods have
CC applicability in developing diagnostic tests and therapeutic treatments
CC for demyelinating diseases. The protein is useful for studying the
CC expression and function of SCN2B and expressing SCN2B protein for use in
CC screening for candidate drugs to treat diseases related to SCN2B
CC activity. The polymorphism and haplotype data are useful for validating
CC whether SCN2B is a suitable target for drugs to treat demyelinating
CC diseases, screening for such drugs and reducing bias in clinical trials.
CC The haplotyping method is useful to validate SCN2B as a candidate target
CC for treating a specific condition or disease predicted to be associated
CC with SCN2B activity. A recombinant non-human organism transformed or
CC transfected with the polypeptide is useful for studying expression of the
CC SCN2B isogenes in vivo, for in vivo screening and testing of drugs
CC against SCN2B protein and for testing the efficacy of therapeutic agents

CC and compounds for demyelinating diseases in a biological system. This
CC sequence is used during the detection of polymorphisms of the SCN2B gene
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGCG 8
Db 4 GGCGGCG 10

RESULT 631
AAD25219
ID AAD25219 standard; DNA; 10 BP.
XX
AC AAD25219;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human homeo box D3 (HOXD3) gene polymorphism detecting primer #18.
XX
KW Human; homeo box D3; HOXD3; polymorphism; developmental disorder;
KW haplotype; HT; allele-specific oligonucleotide; ASO; tumour; therapy;
KW drug screening; cytostatic; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190127-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US016982.
XX
PR 25-MAY-2000; 2000US-0207076P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Duda A, Kazemi A, Koshy B, Kumar AM;
XX
DR WPI; 2002-075363/10.
XX
PT New genetic variants of Homeo Box D3 for studying expression and function
PT of the protein, and for screening drugs to treat diseases e.g.
PT developmental disorders and tumors.
XX
PS Claim 18; Page 13; 66pp; English.
XX
CC The invention relates to genetic variants of the homeo box D3 (HOXD3)
CC gene. HOXD3 gene includes 9 polymorphic sites PS1-PS9. Haplotypes (HTS)
CC or haplotype pairs (HP) for PS1-PS9 in the HOXD3 gene are useful for
CC improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC HOXD3 activity, e.g., developmental disorders and tumours. HOXD3 isogene
CC is useful in studying the expression and function of HOXD3 and in
CC expressing HOXD3 protein for use in screening for candidate drugs to
CC treat diseases related to HOXD3 activity and in studying the effect of
CC the variation on the biological activity of HOXD3 as well as on the
CC binding affinity of candidate drugs targeting HOXD3 for the treatment of
CC developmental disorders and tumours. An antibody against HOXD3 is useful
CC in a variety of diagnostic and prognostic formats and therapeutic
CC methods. A recombinant non-human organism is useful in studying
CC expression of the HOXD3 isogenes in vivo. Allele-specific
CC oligonucleotides (ASO) are useful as probes and primers and for assaying
CC a polymorphism in the target region. The present sequence is a primer
CC used for detecting human HOXD3 gene polymorphisms
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
Db 3 GGCGGCA 9

RESULT 632
ABN80657/c
ID ABN80657 standard; DNA; 10 BP.
XX
AC ABN80657;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P450(cytochrome) oxidoreductase ASO primer extension oligo #45.
XX
KW Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
KW single nucleotide polymorphism; flavoprotein; enzyme;
KW primer extension oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200226768-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-US030877.
XX
PR 29-SEP-2000; 2000US-0236449P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;
XX
DR WPI; 2002-394236/42.
XX
PT New genetic variants comprising haplotypes of the P450 (cytochrome)
PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug
PT screening protocols for compounds targeting POR.
XX
PS Claim 16; Page 15; 141pp; English.
XX
CC The present invention provides the protein, gene and cDNA sequences of
CC human P450(cytochrome) oxidoreductase POR, and single nucleotide
CC polymorphisms (SNPs) identified therein. The sequences can be used to
CC haplotype the POR gene of an individual, and to establish whether POR is
CC a suitable target for drugs to treat cancer and disorders associated with
CC impaired protein synthesis in cells. The present sequence is an allele
CC specific primer extension oligonucleotide for the coding sequences of the
CC invention
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
Db 7 GGCGGCA 1

RESULT 633
ABV78532/c
ID ABV78532 standard; cDNA; 10 BP.
XX
AC ABV78532;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:243.
XX

KW SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW activated T cell; T lymphocyte; immune response; expression pattern;
KW preferential expression; immune disorder; EST; expressed sequence tag;
KW ss.
XX
OS Homo sapiens.
XX
PN JP2002186482-A.
XX
XX 02-JUL-2002.
PD
XX
PF 19-DEC-2000; 2000JP-00385816.
XX
XX 19-DEC-2000; 2000JP-00385816.
PR
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX WPI; 2002-594261/64.
DR
XX Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases.
XX
XX
PS Claim 19; Page 12; 60pp; Japanese.
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are expressed in activated human Th1
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC lying nearest to the polyA region of cDNAs derived from a variety of
CC genes. These tags serve to uniquely identify each transcript and can thus
CC be used to analyse the pattern of gene expression in particular cell
CC types. The invention also relates to proteins encoded by the genes
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC inhibitors of the expression of groups of genes that are expressed in
CC either or both the two cell types. Groups of genes expressed in Th1
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC representing 171 genes which are more highly expressed in Th1 cells
CC compared with Th2 cells
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
Db 10 CGGCATC 4

RESULT 634
ABV84235/C
ID ABV84235 standard; cDNA; 10 BP.
XX
AC ABV84235;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human chronic hepatitis C tissue overexpressed gene SAGE tag #45.
XX
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; differential expression; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
XX 30-JUL-2002.
PD
PF 19-JAN-2001; 2001JP-00012328.
XX

PR 19-JAN-2001; 2001JP-00012328.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes.
XX
XX Claim 1; Page 11; 139pp; Japanese.
PS
XX
CC The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis C
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84191-ABV84290 are SAGE tags representing the 100 most highly
CC expressed genes out of those genes which are overexpressed in chronic
CC hepatitis C liver tissue compared with normal liver tissue
XX
SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7
Db 8 CGGCGGG 2

RESULT 635
ABV84447/C
ID ABV84447 standard; cDNA; 10 BP.
XX
AC ABV84447;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human HCC overexpressed gene SAGE tag #257.
XX
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW expression pattern; differential expression; ss.
XX
OS Homo sapiens.
XX
PN JP2002209591-A.
XX
XX 30-JUL-2002.
PD
XX 19-JAN-2001; 2001JP-00012328.
PF
XX
PR 19-JAN-2001; 2001JP-00012328.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX WPI; 2002-631294/68.
DR
XX Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes.

XX Claim 19; Page 17; 139pp; Japanese.

PS The invention relates to SAGE (serial analysis of gene expression) tags

XX representing groups of genes which are differentially expressed in human

CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced

CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.

CC The SAGE tags of this invention consist of a sequence of 10 nucleotides

CC located downstream of the 5'-CATC-3' sequence motif lying nearest to the

CC polyA region of cDNAs derived from a variety of genes. These tags serve

CC to uniquely identify each transcript and can thus be used to analyse the

CC pattern of gene expression in particular cell types. The invention also

CC relates to proteins encoded by the genes expressed in chronic hepatitis C

CC liver tissue or HCC, antibodies against these proteins, and inhibitors of

CC the expression of groups of genes that are overexpressed in chronic

CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed

CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and

CC treatment of these diseases. Such genes, inhibitors of their expression

CC or activity, and antibodies against the gene products may be used in the

CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences

CC ABV84391-ABV84490 are SAGE tags representing the 100 most highly

CC expressed genes out of those genes which are overexpressed in

CC hepatocellular carcinoma compared with normal liver tissue

XX

SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7

Db 8 CGGCGGG 2

RESULT 636

ABK23563/C

ID ABK23563 standard; DNA; 10 BP.

XX

AC ABK23563;

XX

DT 09-APR-2002 (first entry)

XX

DE Transcript tag DNA sequence #152 induced or suppressed by N-myc.

XX

KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;

KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;

KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.

XX

OS Homo sapiens.

XX

PN WO200185941-A2.

XX

PD 15-NOV-2001.

XX

PF 11-MAY-2001; 2001WO-NL000361.

XX

PR 11-MAY-2000; 2000EP-00201698.

PR 29-JUN-2000; 2000EP-00202284.

XX

PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.

XX

PI Versteeg R, Caron HN;

XX

DR WPI; 2002-066603/09.

XX

PT A new nucleic acid library of myc-dependent downstream genes capable of

PT supporting a neoplastic characteristic of cancer is useful to find new

PT therapies and diagnoses for cancer.

XX

PS Disclosure; Page 53; 69pp; English.

XX

CC The present invention relates to a nucleic acid library comprising myc-

CC dependent downstream genes or their functional fragments essentially

CC capable of supporting a neoplastic character of cancer such as growth,

CC invasion or spread. These myc target or tag sequences are identified by

CC SAGE (serial analysis of gene expression). The library is useful to find

CC new diagnoses and treatments for cancer. The invention is also useful to

CC enhance production of recombinant proteins in a production system with

CC high expression of endogenous or transfected myc oncogenes. ABK23412-

CC ABK23828 represent transcript tag DNA sequences that are activated or

CC repressed by N-myc in human neuroblastoma

XX

SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14

Db 10 CGGCATC 4

RESULT 637

ABK81324

ID ABK81324 standard; DNA; 10 BP.

XX

AC ABK81324;

XX

DT 13-AUG-2002 (first entry)

XX

DE Human ADMR gene allele-specific oligonucleotide PCR primer #21.

XX

KW Human; G protein-coupled receptor similar to the adrenomedullin receptor;

KW ADMR; haplotyping; haplotype pair; congestive heart failure; primer; ss;

KW arterial hypertension; pulmonary hypertension; renal failure; sepsis;

KW chromosome 12; single nucleotide polymorphism; PCR.

XX

OS Homo sapiens.

XX

PN WO200226770-A2.

XX

PD 04-APR-2002.

XX

PF 01-OCT-2001; 2001WO-US030879.

XX

PR 29-SEP-2000; 2000US-0236570P.

XX

PA (GENA-) GENAISANCE PHARM INC.

XX

PI Choi JY, Lee HH, Shah N;

XX

DR WPI; 2002-435192/46.

XX

PT Novel G-protein coupled receptor similar to the adrenomedullin receptor

PT gene, useful therapeutically and in screening for drugs targeting

PT receptor polypeptide.

XX

PS Claim 16; Page 14; 78pp; English.

XX

CC The invention relates to single nucleotide polymorphisms in the gene

CC encoding the human G protein-coupled receptor similar to the

CC adrenomedullin receptor (ADMR) polypeptide. A method for haplotyping the

CC ADMR gene in an individual comprises identifying the nucleotide at one or

CC more polymorphic sites and determining whether one of the copies of the

CC gene is defined by one of the ADMR haplotypes given in the specification

CC or whether both copies are defined by a haplotype pair. This method is

CC useful in genotyping, whereby all possible haplotype pairs can be

CC assigned to specific genotypes. An association between a trait and a

CC haplotype or haplotype pair of the ADMR gene can be identified by

CC comparing the frequency of the haplotype or haplotype pair in a

CC population exhibiting the trait with the frequency of the haplotype or

CC haplotype pair in a reference population, where a higher haplotype

CC frequency in the trait population indicates the trait is associated with

CC the haplotype or haplotype pair. ADMR and its corresponding DNA are used

CC for studying the expression and function of ADMR, for use in screening
CC for candidate drugs to treat diseases related to ADMR activity, such as
CC congestive heart failure, arterial hypertension, pulmonary hypertension,
CC renal failure, and sepsis. Sequences ABK81304-ABK81325 represent allele-
CC specific oligonucleotide PCR primers used to detect ADMR gene
CC polymorphisms
XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 1 GGCGGGC 7

RESULT 638
AAS95686
ID AAS95686 standard; DNA; 10 BP.
XX
AC AAS95686;
XX
DT 14-FEB-2002 (first entry)
XX
DE Superoxide dismutase 1 (SOD1) allele-specific oligonucleotide #27.
XX
KW Superoxide dismutase 1; soluble amyotrophic lateral sclerosis 1 (adult);
KW haplotyping; SOD1; allele-specific oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200185741-A2.
XX
PD 15-NOV-2001.
XX
PF 07-MAY-2001; 2001WO-US014772.
XX
PR 05-MAY-2000; 2000US-0202491P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Bentivegna SC, Kliem SE, Koshy B, Parks KE;
XX WPI; 2002-0555578/07.
DR
XX
PT Isolated human superoxide dismutase 1 (SOD1) soluble polynucleotide,
PT useful for screening therapeutic compounds, comprises a sequence which is
PT a polymorphic variant of reference sequence for the SOD1 gene or its
PT fragment.
XX
PS Claim 17; Page 13; 70pp; English.
XX
CC The invention relates to an isolated human superoxide dismutase 1,
CC soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1) polynucleotide
CC (I) comprising a sequence which is a polymorphic variant of a reference
CC sequence for the SOD1 gene. Haplotyping the SOD1 gene of an individual,
CC involves: (a) determining whether the individual has one of the SOD1
CC haplotypes or haplotype pairs given in the specification; or (b)
CC determining for one copy of the SOD1 gene present in the individual, the
CC identity of the nucleotide at two or more polymorphic sites selected from
CC PSI-7. The method is useful for determining whether an individual has a
CC haplotype or haplotype pairs defined in the specification. The method is
CC also useful for improving the efficacy and reliability of several steps
CC in the discovery and development of drugs for treating diseases
CC associated with SOD1 activity, e.g., amyotrophic lateral sclerosis, and
CC to validate SOD1 as a candidate agent for treating a specific condition
CC or disease associated with SOD1 activity. It can further be used in the
CC design of clinical trials of candidate drugs for treating a specific
CC condition or disease predicted to be associated with SOD1 activity. (I)
CC is useful in studying the expression and function of SOD1, and in
CC expressing SOD1 protein for use in screening for candidate drugs to treat

CC diseases related to SOD1 activity. AAS95660-AAS95710 represent human
CC superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
CC (SOD1) allele-specific oligonucleotides and related PCR primers as
CC described in the method of the invention
XX
SQ Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCGGGC 11
Db 2 GGCGGGC 8

RESULT 639
ABA93354
ID ABA93354 standard; DNA; 10 BP.
XX
AC ABA93354;
XX
DT 22-APR-2002 (first entry)
XX
DE Human ACAA1 gene polymorphism detection primer SEQ ID NO:69.
XX
KW Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22;
KW peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;
KW single nucleotide polymorphism; polymorphic variant; enzyme; probe;
KW primer; allele specific oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200187903-A2.
XX
PD 22-NOV-2001.
XX
PF 03-MAY-2001; 2001WO-US014330.
XX
PR 18-MAY-2000; 2000US-0205022P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (DUDA/) DUDA A E.
XX
PI Chew A, Koshy B;
XX
DR WPI; 2002-164134/21.
XX
PT Isolated polynucleotide, comprising a polymorphic variant of the acetyl-
PT Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
PT gene useful for providing haplotype information and in therapy for
PT treating related disorders.
XX
PS Claim 17; Page 14; 93pp; English.
XX
CC The present invention describes a polypeptide (I) which is a polymorphic
CC variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal 3-
CC oxoacyl-Coenzyme A thiolase) ACAA1 protein (AB05516). ACAA1 is located
CC on chromosome 3p23-p22. (I) can be encoded by ABA93286 (or ABA93288)
CC where the sequence comprises one of the haplotypes shown in Table 4 or
CC one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are
CC given in the specification. The polynucleotide encoding ACAA1 can be used
CC for providing haplotype and genotype information of an individual.
CC Furthermore, the polynucleotide is useful for the treatment of disorders
CC related to its abnormal expression or function. ABA93289 to ABA93383
CC represent allele specific oligonucleotides (ASOs) which are used in the
CC detection of polymorphisms in the human ACAA1 gene
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCGGC 11
| | | | |
Db 1 GGCGGC 7

RESULT 640
AAD26959
ID AAD26959 standard; DNA; 10 BP.
XX
AC AAD26959;
XX
DT 09-APR-2002 (first entry)
XX
DE Oligonucleotide used to isolate hITF probe by PCR.
XX
KW Intestinal trefoil factor; ITF; inflammatory bowel disease; therapy;
KW bacterial infection; peptic ulcer; radiation surgery; antiulcer;
KW antiinflammatory; ss.
XX
OS Unidentified.
XX
PN US6316218-B1.
XX
PD 13-NOV-2001.
XX
PF 27-JAN-1998; 98US-00056868.
XX
PR 14-FEB-1991; 91US-00655965.
PR 13-FEB-1992; 92US-00837192.
PR 25-MAR-1993; 93US-00037741.
PR 02-FEB-1994; 94US-00191352.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Podolsky DK;
XX
DR WPI; 2002-121020/16.
XX
PT A nucleic acid encoding an intestinal trefoil factor is useful to treat
PT peptic ulcers and inflammatory bowel disease, and to protect the
PT intestine against injury from insults such as bacterial infection and
PT radiation surgery.
XX
PS Disclosure; Col 7; 17pp; English.
XX
CC The present invention relates to an isolated nucleic acid that encodes an
CC intestinal trefoil factor (ITF) polypeptide. The intestinal trefoil
CC factor can be used to treat peptic ulcers and inflammatory bowel diseases
CC and to protect the intestinal tract from injury caused by bacterial
CC infection, radiation surgery or other insults. It may also be used to
CC protect and stabilise other proteins in the digestive tract. The present
CC sequence is an oligonucleotide used in the isolation of human ITF (hITF)
CC probe by PCR
XX
SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCGGC 11
| | | | |
Db 1 GGCGGC 7

RESULT 641
AAD44209
ID AAD44209 standard; cDNA; 10 BP.
XX
AC AAD44209;
XX
DT 13-DEC-2002 (first entry)

XX
DE Human TANGO 239 form 1 cDNA 3' end fragment.
XX
KW TANGO protein; vaccine; chromosomal mapping; antisense gene therapy;
KW forensic biology; predictive medicine; cytostatic; pharmacogenomic;
KW tissue typing; human; ss.
XX
OS Homo sapiens.
XX
PN US2002055139-A1.
XX
PD 09-MAY-2002.
XX
PF 01-MAR-2001; 2001US-00796858.
XX
PR 30-DEC-1998; 98US-00223094.
PR 30-DEC-1998; 98US-00223546.
PR 30-DEC-1998; 98US-00224246.
PR 14-MAY-1999; 99US-00312359.
PR 18-JUN-1999; 99US-00336536.
PR 29-JUN-1999; 99US-00342687.
PR 30-JUL-1999; 99US-00365164.
PR 20-SEP-1999; 99US-00399723.
PR 23-DEC-1999; 99US-00471179.
PR 29-DEC-1999; 99US-00474071.
PR 29-DEC-1999; 99US-00474072.
PR 15-MAY-2000; 2000US-00572002.
PR 19-JUN-2000; 2000US-00597993.
PR 22-JUN-2000; 2000US-00599596.
PR 29-JUN-2000; 2000US-00606565.
PR 31-JUL-2000; 2000US-00630334.
PR 20-SEP-2000; 2000US-00665666.
XX
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIG/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
XX
PI Holtzman DA, Sharp JD, Leiby KR, Bossone S, Pan Y, Barnes TM;
PI Fraser CC, Wrighton N, Myers PS, Kingsbury G;
XX
DR WPI; 2002-453953/48.
XX
PT New isolated nucleic acid encoding a TANGO polypeptide, for use as a
PT modulating agent for regulating cellular processes and for use in a
PT vaccine.
XX
PS Disclosure; Page 12; 206pp; English.
XX
CC The invention relates to TANGO polypeptide and its corresponding nucleic
CC acid sequence. TANGO protein is used to identify a compound which binds
CC to it that can be used for modulating its activity. It is also used to
CC produce an antibody. The antibody is used to detect the presence of the
CC polypeptide in a sample. TANGO DNA and protein are useful as modulating
CC agents in regulating cellular processes. They can be used in vaccines.
CC TANGO DNA and protein and its antibody are used in e.g. chromosomal
CC mapping, tissue typing, forensic biology, predictive medicine,
CC pharmacogenomics and treatment methods. TANGO DNA is used in antisense
CC gene therapy. The present sequence is human TANGO 239 form 1 cDNA
CC fragment
XX
SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db 1 GGGCGGC 7

RESULT 642
AAD32318
ID AAD32318 standard; DNA; 10 BP.
XX AC AAD32318;
XX DT 18-JUN-2002 (first entry)
XX DE Human neurotrophin 3 (NTF3) gene polymorphism detecting primer #4.
XX KW Human; genetic variant; neurotrophin 3; NTF3; haplotyping; genotyping;
KW nervous system disorder; congenital heart defect; gene therapy;
KW therapeutic; polymorphism; primer; ss.
XX OS Homo sapiens.
XX PN WO200212499-A2.
XX PD 14-FEB-2002.
XX PF 06-AUG-2001; 2001WO-US024665.
XX PR 04-AUG-2000; 2000US-0223208P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Kliem SE, Koshy B, Lanz EM;
XX WPI; 2002-269092/31.
XX PT Novel polymorphic variants of neurotrophin 3 (NTF3), useful for studying
PT the expression and function of NTF3, and for screening candidate drugs to
PT treat nervous system disorders and congenital heart defects.
XX PS Claim 19; Page 13; 60pp; English.
XX CC The present invention relates to genetic variants of human neurotrophin
CC (NTF) 3 gene. The invention also relates to compositions and methods for
CC haplotyping and/or genotyping the NTF3 gene in an individual. Sequences
CC of the invention are useful for studying the expression and function of
CC NTF3 protein for use in screening for candidate drugs to treat diseases
CC related to NTF3 activity. The polymorphism and haplotype data is useful
CC for validating whether NTF3 is a suitable target for drugs to treat
CC nervous system disorders and congenital heart defects, screening for such
CC drugs and reducing bias in clinical trials of such drugs. They are also
CC useful for therapeutic purposes. The haplotyping method is useful for
CC improving the efficiency and outcome of several steps in the discovery
CC and development of drugs for treating diseases associated with NTF3
CC activity such as nervous system disorders and congenital heart defects.
CC It is also useful for validating NTF3 as a candidate target for treating
CC a specific condition or disease predicted to be associated with NTF3
CC activity. The method is also useful for screening compounds to treat a
CC specific condition or disease predicted to be associated with NTF3
CC activity. Sequences of the invention are also used in gene therapy. The
CC present DNA sequence is a primer used to detect human NTF3 gene
CC polymorphisms
XX SQ Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGCGGC 8
Db 4 GGGCGGC 10

RESULT 643
ABK93089
ID ABK93089 standard; DNA; 10 BP.
XX AC ABK93089;
XX DT 22-AUG-2002 (first entry)
XX DE Human cancer related gene associated primer #1.
XX KW Human; cancer; DNA array; gene expression analysis; primer; PCR; ss.
XX OS Homo sapiens.
XX PN JP2002058495-A.
XX PD 26-FEB-2002.
XX PF 22-AUG-2000; 2000JP-00255737.
XX PR 22-AUG-2000; 2000JP-00255737.
XX PA (HITA) HITACHI LTD.
XX DR WPI; 2002-398777/43.
XX PT A DNA array that observes the expression of cancer related genes is
PT useful for the elucidation of the action mechanism of anticancer agents.
XX PS Disclosure; Page 8; 71pp; Japanese.
XX CC The invention relates to a DNA array for identifying cancer related
CC genes. The DNA array comprises: (a) statistically significantly higher
CC results of over 10% in homology search of a DNA molecule describing
CC different genes or a complementary DNA (cDNA); (b) statistically
CC significantly higher results (p value) of over 10% in homology search
CC with human Alu sequence; (c) difference of melting temperature of the DNA
CC fragment and hybridisation temperature at 30 degree C or less; (d) the
CC DNA fragment prepared by immobilisation of a DNA short sequence with a
CC specific higher order structure; and (e) the DNA fragment without short
CC repetitive sequence. The array is used in elucidation of the action
CC mechanism of anticancer agents. ABK92989-ABK93090 represent human cancer
CC related genes and associated primers of the invention
XX SQ Sequence 10 BP; 0 A; 2 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCGGC 11
Db 1 GGGCGGC 7

RESULT 644
AAS99398
ID AAS99398 standard; DNA; 10 BP.
XX AC AAS99398;
XX DT 12-MAR-2002 (first entry)
XX DE Aldehyde dehydrogenase 5 family, member A1, oligonucleotide #91.
XX KW Aldehyde dehydrogenase 5 family member A1; ALDH5A1;
KW succinate-semialdehyde dehydrogenase; gene therapy; primer;
KW antisense technology; primer extension oligonucleotide;
KW 4-hydroxybutyric aciduria; metabolic disease; transgenic animal; ss.
XX OS Synthetic.
XX PN WO200190119-A2.

XX 29-NOV-2001.
PD
XX
XX 21-MAY-2001; 2001WO-US016558.
PF
XX
XX 19-MAY-2000; 2000US-0205849P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Kliem SE, Koshi B, Tanguay DA;
PI
XX WPI; 2002-089912/12.
DR
XX
XX New genetic variants of human aldehyde dehydrogenase 5 family, member A1, member A1, ALDH5A1 gene for treating metabolic diseases and for expressing ALDH5A1 protein useful in identifying drugs to treat 4-hydroxybutyric aciduria.
PT
PT
XX
XX Claim 18; Page 14; 151pp; English.
PS
XX
CC The invention describes an isolated polynucleotide comprising a nucleotide sequence which is a polymorphic variant of a reference sequence for the aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1) gene or its fragment. The polypeptide is useful for screening for drugs targeting it by contacting the ALDH5A1 polymorphic variant with a candidate agent and assaying for binding activity. The polypeptide and haplotypes are useful for identifying acting an association between a trait such as a clinical response to a drug targeting ALDH5A1 and a haplotype ALDH5A1 gene. Transgenic animals are also useful for studying expression of the ALDH5A1 isogenes in vivo, for in vivo screening and testing of drugs against ALDH5A1 protein and for testing the efficacy of therapeutic agents and compounds for 4-hydroxybutyric aciduria and metabolic diseases in a biological system. Antibodies are useful for diagnostic and prognostic formats and therapeutic methods, for immunoprecipitating the polypeptide from solution, for detecting ALDH5A1 protein isoforms in biological samples, frozen tissue sections, for use in immunocytochemical, immunohistochemical and immunofluorescence techniques. The polynucleotide is useful for gene therapy and antisense gene therapy. This sequence is a primer extension oligonucleotide used to detect polymorphisms in the ALDH5A1 gene described in the method of the invention

XX
SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;
SQ
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 6 GGCGGCA 12
Db 3 GGCGGCA 9
RESULT 645
AAD26797/c
ID AAD26797 standard; DNA; 10 BP.
XX
AC AAD26797;
XX
XX 09-APR-2002 (first entry)
XX
XX Primer #4 to detect human SNAP29 gene polymorphisms.
DE
XX
XX Human; synaptosomal-associated protein 29 kD; SNAP29 protein; haplotyping; genotyping; membrane trafficking related disorder; gene therapy; polymorphism; primer; ss.
KW
KW
XX Homo sapiens.
OS
XX WO200190126-A2.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 23-MAY-2001; 2001WO-US016938.
PF

XX 23-MAY-2000; 2000US-0206529P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Kazemi A, Koshi B, Tanguay DA;
PI
XX WPI; 2002-089916/12.
DR
XX
XX Novel isolated polynucleotide, a polymorphic variant of synaptosomal-associated protein, 29 kD (SNAP29) gene useful for expressing SNAP29 protein isoform to screen drugs to treat SNAP29 activity-related disease.
PT
PT
XX
XX Claim 18; Page 14; 115pp; English.
PS
XX
CC The invention relates to genetic variants of human synaptosomal-associated protein, 29 kD (SNAP29) gene. The invention also relates to compositions and methods for haplotyping and/or genotyping the SNAP29 gene in an individual. Polynucleotides of the invention are useful for studying the expression and function of SNAP29 and expressing SNAP29 protein for use in screening candidate drugs to treat diseases related to SNAP29 activity. They are also used in gene therapy. The genotyping method is useful for determining if an individual has one of haplotype or haplotype pairs. The polymorphism and haplotype data is useful for validating whether SNAP29 is a suitable target for drugs to treat disorders related to membrane trafficking, screening for such drugs and reducing bias cells in clinical trials of such drugs. The present sequence is a primer for detecting human SNAP29 gene polymorphisms

XX
SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 6 GGCGGCA 12
Db 7 GGCGGCA 1
RESULT 646
ADG28269
ID ADG28269 standard; DNA; 10 BP.
XX
XX AC ADG28269;
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Human Myo/V1 protein-related NFKappaB regulation site SeqID344.
DE
XX
XX cardiac-associated protein; Myo/V1 protein; MP; cardiant; vasotropic; immunosuppressive; vulnerary; NFKappaB p50; NFKappaB p65;
KW
KW cardiovascular disease; cardiac hypertrophy; myocardial infarction; ischaemia; reperfusion injury; heart transplantation;
KW anti-ageing treatment; human; ds.
XX
XX Homo sapiens.
OS
XX WO200245659-A2.
PN
XX
XX 13-JUN-2002.
PD
XX
XX 26-OCT-2001; 2001WO-US051272.
PF
XX
XX 27-OCT-2000; 2000US-0243985P.
PR
XX
XX (BAYU) BAYLOR COLLEGE MEDICINE.
PA
XX Sivasubramanian N, Knuefermann P, Mann DL;
PI
XX WPI; 2002-537532/57.
DR
XX
XX Novel dominant negative mutant sequence or constitutively active mutant

PD 13-JUN-2002.
XX
PF 26-OCT-2001; 2001WO-US051272.
XX
PR 27-OCT-2000; 2000US-0243985P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Sivasubramanian N, Knuefermann P, Mann DL;
XX WPI; 2002-537532/57.
DR
XX Novel dominant negative mutant sequence or constitutively active mutant
PT sequence of Myo/VI polypeptide, useful for treating cardiovascular
PT disorders and inhibiting formation of NFkappaB homodimers.
XX
PS Claim 45; SEQ ID NO 34; 217pp; English.
XX
CC This invention relates to a novel dominant negative or constitutively
CC active mutant sequence of the cardiac-associated Myo/VI protein (MP). The
CC invention may be useful for the development of compounds with a cardiant,
CC vasotropic, immunosuppressive or vulnerary activity through the
CC inhibition of formation of NFkappaB p50 or NFkappaB p65 homodimers. The
CC invention may be useful for the development of treatments for
CC cardiovascular disease including cardiac hypertrophy, myocardial
CC infarction, ischaemia/reperfusion injury and heart transplantation, in a
CC mammal, for anti-ageing treatment, for inhibiting formation of NFkappaB
CC p50 homodimers or NFkappaB p65 homodimers in a cell of a mammal and for
CC reducing formation of NFkappaB p65 homodimers in a cell of a mammal.
XX
SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db | | | | | | |
1 GGGCGGC 7

RESULT 652
ABZ80704
ID ABZ80704 standard; DNA; 10 BP.
XX
AC ABZ80704;
XX
DT 07-JUL-2003 (first entry)
XX
DE UME6 consensus binding sequence #2.
XX
KW binding sequence; ss; UME6; meiosis; transcriptional regulation; MEME;
KW gene network; quantitative disruptant data library; gene expression;
KW gene regulation; Multiple Expectation-Maximization for motif Elicitation;
KW consensus.
XX
OS Homo sapiens.
XX
PN WO2003027262-A2.
XX
PD 03-APR-2003.
XX
PF 26-SEP-2002; 2002WO-US031093.
XX
PR 26-SEP-2001; 2001US-0325016P.
PR 29-NOV-2001; 2001US-0334230P.
PR 29-NOV-2001; 2001US-0334255P.
PR 29-NOV-2001; 2001US-0334372P.
PR 08-APR-2002; 2002US-0370824P.
PR 19-JUL-2002; 2002US-0397458P.
XX
PA (GENE-) GENE/NETWORKS INC.
XX

PI Imoto S, Goto T, Miyano S, Tashiro K, De Hoon M, Savoie CJ;
PI Kuhara S;
XX
DR WPI; 2003-371918/35.
XX
PT Gene network construction, involves creating gene expression matrix based
PT on expression result of gene disruption, using Bayesian computational
PT model such that BNRC criterion is minimum.
XX
PS Disclosure; Page 11; 161pp; English.
XX
CC The invention relates to a method of constructing gene networks by
CC providing a quantitative disruptant data library for a set of genes of an
CC organism, including expression results of disruption of each gene,
CC quantifying average effect and variability measure of each disruption for
CC every other gene, creating gene expression matrix, generating network of
CC relationship between genes, and determining differential expression of
CC gene groups. The method is useful for constructing gene network for genes
CC of organism to predict putative therapeutic targets The method provides
CC internal control and quantitative measurement of the direct effects of
CC the presence or absence of the gene on the expression of other genes.
CC Therefore selection of disruptant experiments to maximize the elucidation
CC of gene control relationships is achieved to generate useful gene
CC regulatory information. To illustrate the invention, Multiple Expectation
CC -Maximization for motif Elicitation (MEME) was performed on 34 genes
CC controlled by UME6, a global transcriptional regulator of meiotic genes.
CC This consensus sequence was found in 32.4% of genes examined. This
CC sequence is defined as the binding site for a repressor of the CAR1 gene
XX
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db | | | | | | |
2 GGGCGGC 8

RESULT 653
ACC41654
ID ACC41654 standard; DNA; 10 BP.
XX
AC ACC41654;
XX
DT 21-MAY-2003 (first entry)
XX
DE Zinc finger protein DNA-binding domain target sequence SEQ ID NO:201.
XX
KW Zinc finger domain; zinc finger; zinc finger binding domain; probe;
KW chimeric nucleic acid; library; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO2003016571-A1.
XX
PD 27-FEB-2003.
XX
PF 17-AUG-2002; 2002WO-KR001560.
XX
PR 17-AUG-2001; 2001US-0313402P.
PR 22-APR-2002; 2002US-0374355P.
XX
PA (TOOL-) TOOLGEN INC.
XX
PI Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;
XX WPI; 2003-268344/26.
DR
XX New library comprising polypeptides having zinc finger domains, useful
PT for producing chimeric nucleic acids.
XX

PS Claim 40; Page 101; 234pp; English.

XX The present invention describes a library comprising polypeptides. Each

CC polypeptide comprises a first or second zinc finger domain. The domains

CC of each polypeptide are identical to a zinc finger domain from a

CC naturally occurring protein and either do not occur in the same naturally

CC occurring protein or occur in the same naturally occurring protein in a

CC different configuration than in the polypeptide. The domains vary among

CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)

CC generating an artificial zinc finger polypeptide that specifically binds

CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc

CC finger polypeptide that specifically recognises a target DNA site. The

CC library can be used for producing chimeric nucleic acids. ACC41551 to

CC ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid

CC sequences given in the exemplification of the present invention

XX

SQ Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7

Db 2 CGGCGGG 8

RESULT 654

ABT14274

ID ABT14274 standard; DNA; 10 BP.

XX

AC ABT14274;

XX

DT 20-FEB-2003 (first entry)

XX

DE Nucleic acid PCR amplification method-related RAPD PCR primer #44.

XX

KW Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;

KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.

XX

OS Unidentified.

XX

PN WO200281743-A2.

XX

PD 17-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-GB001489.

XX

PR 02-APR-2001; 2001GB-00008182.

XX

PA (HAMI/) HAMILL B.

XX

PI Hamill B;

XX

DR WPI; 2003-075484/07.

XX

Amplification of nucleotide sequences from polynucleotides by chain

extension of oligonucleotide primers, comprises 2 oligonucleotides in

solution, 2 attached to supports and both share complementary sequences.

Disclosure; Fig 17; 60pp; English.

The invention comprises a method for the PCR amplification of nucleic

acids. The method involves a set of primers, where two of the primers are

in solution and at least two other primers are attached to a solid

support. The method of the invention can be used for the analysis of a

nucleic acid or a mixture of nucleic acids, including: single-stranded

DNA molecules, double-stranded DNA molecules and mRNA molecules. The

present DNA sequence represents a random amplified polymorphic DNA (RAPD)

PCR primer of the invention

Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCATCG 15

Db 1 GGCATCG 7

RESULT 655

ABT14362/c

ID ABT14362 standard; DNA; 10 BP.

XX

AC ABT14362;

XX

DT 20-FEB-2003 (first entry)

XX

DE Nucleic acid PCR amplification method-related RAPD PCR primer #132.

XX

KW Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;

KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.

XX

OS Unidentified.

XX

PN WO200281743-A2.

XX

PD 17-OCT-2002.

XX

PF 28-MAR-2002; 2002WO-GB001489.

XX

PR 02-APR-2001; 2001GB-00008182.

XX

PA (HAMI/) HAMILL B.

XX

PI Hamill B;

XX

DR WPI; 2003-075484/07.

XX

Amplification of nucleotide sequences from polynucleotides by chain

extension of oligonucleotide primers, comprises 2 oligonucleotides in

solution, 2 attached to supports and both share complementary sequences.

Disclosure; Fig 17; 60pp; English.

The invention comprises a method for the PCR amplification of nucleic

acids. The method involves a set of primers, where two of the primers are

in solution and at least two other primers are attached to a solid

support. The method of the invention can be used for the analysis of a

nucleic acid or a mixture of nucleic acids, including: single-stranded

DNA molecules, double-stranded DNA molecules and mRNA molecules. The

present DNA sequence represents a random amplified polymorphic DNA (RAPD)

PCR primer of the invention

Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGGCAT 13

Db 8 GCGGCAT 2

RESULT 656

ACA62091

ID ACA62091 standard; DNA; 10 BP.

XX

AC ACA62091;

XX

DT 19-AUG-2003 (first entry)

XX

DE Gustductin alpha subunit cloning associated adaptor #2.

XX Taste; taste modification; gustducin alpha subunit;
KW ligand binding activity; antiligan binding activity;
KW G protein alpha subunit; conserved region; adaptor; ds.
XX
OS Synthetic.
XX
PN US2003013119-A1.
XX
XX 16-JAN-2003.
XX
PD
XX
PF 21-FEB-2001; 2001US-00789996.
XX
PR 09-APR-1992; 92US-00868353.
PR 08-APR-1993; 93US-00045801.
PR 20-MAR-1995; 95US-00407804.
PR 28-JUL-1998; 98US-00124807.
PR 20-OCT-1999; 99US-00421796.
XX
PA (LING-) LANGUAGE CORP.
XX
PI Margolskee RF;
XX
XX WPI; 2003-466043/44.
XX
PT Novel gustducin alpha-subunit polypeptide possessing ligand/antiligan
PT binding activity or immunological property specific to gustducin, for
PT identifying peptide ligand/antiligan of gustducin and taste modifying
PT agent.
XX
PS Example 1; Page 4; 27pp; English.
XX
XX The invention describes a purified and isolated gustducin alpha subunit
CC polypeptide (I), fragment or variant possessing at least one
CC ligand/antiligan binding activity or immunological property specific to
CC gustducin. (I) is useful for identifying a peptide ligand/antiligan of
CC gustducin, by contacting (I) with peptides and isolating peptides which
CC bind to (I), and for identifying taste modifying agent. An antibody is
CC useful for modifying taste which involves delivering Ab to taste receptor
CC cell. The antibody is useful for purifying (I) and for blocking or
CC inhibiting ligand/antiligan binding activities of gustducin. This
CC sequence represents an adaptor used in the cloning of DNA encoding
CC gustducin alpha subunit
XX
SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db |||||
1 GGGCGGC 7

RESULT 657
ACA62967
ID ACA62967 standard; DNA; 10 BP.
XX
AC ACA62967;
XX
DT 26-AUG-2003 (first entry)
XX
DE DNA sequence for addition to 5'end of primer.
XX
KW Corneal epithelium; trefoil protein; intestinal trefoil factor; ITF;
KW spasmolytic peptide; SP; PS2; corneal ulcer; eye surgery;
KW traumatic physical injury; chemical exposure; peptic ulcer disease;
KW ultraviolet light exposure; inflammatory bowel disease; eye disorder;
KW gastrointestinal motility; corneal epithelial wound healing; antiulcer;
XX antiinflammatory; ophthalmological; ds.
OS Synthetic.

XX US6525018-B1.
XX 25-FEB-2003.
XX
PF 17-MAY-1999; 99US-00313434.
XX
PR 17-MAY-1999; 99US-00313434.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Podolsky DK;
XX
DR WPI; 2003-491768/46.
XX
PT Treatment of disruption of corneal epithelium in patient by administering
PT to the eye of the patient trefoil protein including intestinal trefoil
PT factor, spasmolytic peptide, PS2, or their biological fragments.
XX
PS Example 3; Col 13; 31pp; English.
XX
CC The present invention relates to a method for the treatment of a
CC disruption of the corneal epithelium in a patient. The method involves
CC administering to the patient's eye a trefoil protein including intestinal
CC trefoil factor (ITF), spasmolytic peptide (SP), PS2, or their biological
CC fragments. The method is useful for the treatment of a disruption of the
CC corneal epithelium in a patient. It is useful for treating corneal ulcer,
CC or a disorder caused by traumatic physical injury, eye surgery, chemical
CC exposure, or ultraviolet light exposure. It can also be used for treating
CC peptic ulcer diseases, inflammatory bowel diseases, and eye disorders.
CC The use of intestinal trefoil factor alters gastrointestinal motility in
CC a mammal or enhances corneal epithelial wound healing. The present DNA
CC sequence can be added to the 5'end of a primer to engineer a restriction
CC site
XX
SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db |||||
1 GGGCGGC 7

RESULT 658
AAD58326
ID AAD58326 standard; DNA; 10 BP.
XX
AC AAD58326;
XX
DT 20-NOV-2003 (first entry)
XX
DE GC5 primer used in arbitrarily-primed PCR (AP-PCR) analysis.
XX
KW Cell proliferative disorder; central nervous system disorder; infection;
KW gastrointestinal tract disease; respiratory system disease; inflammation;
KW sexual malfunction; ulcerative colitis; psychotic disorder; hypertension;
KW cardiovascular disorder; immune disorder; Hodgkin's disease; drug abuse;
KW behavioural problem; metabolic disorder; Huntington's disease; dementia;
KW skin disorder; cancer; lesion; autism; therapy; arbitrarily-primed PCR;
XX AP-PCR; primer; ss.
OS Unidentified.
XX
PN WO2003064701-A2.
XX
PD 07-AUG-2003.
XX
PF 30-JAN-2003; 2003WO-US003000.
XX
PR 30-JAN-2002; 2002US-0352944P.

```
XX (EPIG-) EPIGENOMICS AG.
PA
XX Sledziewski A, Schweikhardt RG;
PI
XX WPI; 2003-618367/58.
DR
XX
XX Identifying a reliable diagnostic, prognostic or staging marker for
PT phenotypic conditions characterized by altered DNA methylation, e.g.,
PT cancer, comprises obtaining a set of at least two biological samples in
PT each case having genomic DNA.
XX
XX Example 1; Page 43; 87pp; English.
PS
XX The invention relates to a method for identifying a reliable diagnostic,
CC prognostic or staging marker for phenotypic conditions characterised by
CC altered DNA methylation. The method involves obtaining a set of at least
CC two genomic DNA samples, identifying primary differentially methylated
CC CpG dinucleotide sequence positions, selecting a primary differentially
CC methylated CpG dinucleotide sequence position and confirming the class-
CC distinguishable methylation status of the selected sequence position. The
CC method is useful for identifying a reliable diagnostic, prognostic or
CC staging marker for phenotypic conditions characterised by altered DNA
CC methylation e.g cell proliferative disorders, metabolic disorders,
CC central nervous system disorders, immune disorders, cardiovascular
CC disorders e.g. hypertension, disease of the respiratory system, sexual
CC malfunction, dementia, disease of the gastrointestinal tract, skin
CC disorders, lesions, inflammation, infection, drug abuse, behavioural
CC problems, psychotic disorders, Hodgkin's disease, cancer, autism,
CC ulcerative colitis or Huntington's disease. The method is also useful for
CC treating the above mentioned disorders. The present sequence is a primer
CC used in arbitrarily-primed PCR (AP-PCR) analysis. This sequence is used
CC in the exemplification of the invention
XX
SQ Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db |||||
4 GGGCGGC 10

RESULT 659
ADA63669
ID ADA63669 standard; DNA; 10 BP.
XX
AC ADA63669;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #433.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 20; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGGGCA 12
Db |||||
3 GCGGGCA 9

RESULT 660
ADA63670
ID ADA63670 standard; DNA; 10 BP.
XX
AC ADA63670;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #434.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 20; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
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XX (LIUQ/) LIU Q.
PA
XX PI
XX Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 20; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGGGCA 12
Db |||||
3 GCGGGCA 9

RESULT 660
ADA63670
ID ADA63670 standard; DNA; 10 BP.
XX
AC ADA63670;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #434.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 20; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
```

CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GGCGGCA 12
Db 3 GGCGGCA 9
RESULT 661
ADCl7777
ID ADCl7777 standard; DNA; 10 BP.
XX
AC ADCl7777;
XX
DT 18-DEC-2003 (first entry)
XX
DE Monobactam related tethered diene SEQ ID NO:27.
XX
KW ss; monobactam; antibacterial; PBP2a; inhibitor;
KW methicillin resistant Staphylococcus aureus; MRSA; lactam antibiotic.
XX
OS Synthetic.
XX
PN WO2003051314-A2.
XX
PD 26-JUN-2003.
XX
PF 18-DEC-2002; 2002WO-US040739.
XX
PR 18-DEC-2001; 2001US-0340255P.
XX
PA (INVE-) INVENUX INC.
XX
PI Eaton B, Tarasow T, Nieuwlandt D, Dewey T;
XX
DR WPI; 2003-618003/58.
XX
PT New monobactam compounds used as antibacterial agents against e.g.
PT methicillin resistant Staphylococcus aureus.
XX
PS Example 6; SEQ ID NO 27; 64pp; English.
XX
CC The invention relates to novel monobactam compounds. A compound of the
CC invention has antibacterial activity, and acts as a PBP2a inhibitor. The
CC compounds are used as antibacterial agents. The monobactam compounds
CC restore sensitivity of methicillin resistant Staphylococcus aureus to
CC lactam antibiotic by targeting the molecular mechanism of resistance. The
CC present sequence is used in the exemplification of the invention.
XX
SQ Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCGGG 7
Db 4 CGGCGGG 10
RESULT 662
ADFl7248
ID ADFl7248 standard; DNA; 10 BP.
XX
AC ADFl7248;
XX

DT 12-FEB-2004 (first entry)
XX
DE Human intestinal cDNA library associated DNA.
XX
KW antiinflammatory; ophthalmological; virucide; fungicide; antibacterial;
KW eye disorder; intestinal trefoil factor; ITF; spasmodytic peptide; SP;
KW PS2; superficial punctate keratitis; keratitis sicca; trachoma;
KW herpes simplex keratoconjunctivitis; ophthalmic herpes zoster;
KW phlyctenular keratoconjunctivitis; keratoconus; cicatricial pemphigoid;
KW infection; adenovirus; herpes simplex virus; inflammation;
KW conjunctival epithelium; scleral epithelium; digestive tract; human;
KW intestinal cDNA library; ss.
XX
OS Synthetic.
XX
PN US2003186886-A1.
XX
PD 02-OCT-2003.
XX
PF 30-MAY-2003; 2003US-00449456.
XX
PR 12-APR-1996; 96US-00631469.
PR 11-APR-1997; 97WO-US006004.
PR 17-MAY-1999; 99US-00313434.
PR 06-DEC-2002; 2002US-00313642.
PR 19-FEB-2003; 2003US-00362310.
XX
PA (PODO/) PODOLSKY D K.
XX
PI Podolsky DK;
XX
DR WPI; 2003-899226/82.
XX
PT Treatment of eye disorder comprises administration of trefoil protein
PT from intestinal trefoil factor, spasmodytic peptide, PS2 or their
PT biologically active fragments.
XX
PS Example 3; Page 7; 36pp; English.
XX
CC The invention describes a method of treating an eye disorder comprising
CC administering to the eye a trefoil protein from intestinal trefoil factor
CC (ITF), spasmodytic peptide (SP), PS2 or their biologically active
CC fragments. The method is used for treating eye disorders such as
CC superficial punctate keratitis, keratitis sicca, trachoma, herpes simplex
CC keratoconjunctivitis, ophthalmic herpes zoster, phlyctenular
CC keratoconjunctivitis, keratoconus or cicatricial pemphigoid. The eye
CC disorder is caused by an infection of bacteria, virus or fungi. The virus
CC is adenovirus or herpes simplex virus. The eye disorder is inflammation
CC or conjunctival epithelium or inflammation of the scleral epithelium. The
CC method provides a protective effect on the digestive tract, and the ITF
CC promotes the maintenance of mucosal integrity and can also be used to
CC inhibit adhesion or colonisation of the mucosa by Helicobacter pylori.
CC This sequence represents an oligonucleotide associated with the creation
CC of a human intestinal cDNA library for isolation of cDNA encoding human
CC intestinal trefoil factor (ITF). Note: This sequence differs from SEQ ID
CC NO 5 shown in the sequence listing.
XX
SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGCGGGC 11
Db 1 GGCGGGC 7
RESULT 663
ABZ95037
ID ABZ95037 standard; DNA; 10 BP.
XX
AC ABZ95037;

XX 17-OCT-2003 (first entry)
DT Human adenosine A1 receptor antisense fragment no.900.
XX
DE Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 10279; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
| | | | |
Db 2 GGCGGGC 8

RESULT 664
ABZ95027
ID ABZ95027 standard; DNA; 10 BP.
XX
AC ABZ95027;

XX 17-OCT-2003 (first entry)
DT Human adenosine A1 receptor antisense fragment no.890.
XX
DE Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 10269; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
| | | | |
Db 3 GGCGGGC 9

RESULT 665
ABZ95046
ID ABZ95046 standard; DNA; 10 BP.
XX
AC ABZ95046;

XX 17-OCT-2003 (first entry)
DT Human adenosine A1 receptor antisense fragment no.909.
XX
DE
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
PN
XX
PD 31-OCT-2002.
XX
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
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PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 10288; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 1 GGCGGGC 7

RESULT 666
ABZ95816/c
ID ABZ95816 standard; DNA; 10 BP.
XX
AC ABZ95816;

XX 17-OCT-2003 (first entry)
DT Human adenosine A2b receptor antisense fragment no.1674.
XX
DE
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
PN
XX
PD 31-OCT-2002.
XX
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
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XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 11058; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCGGGC 9
Db 9 GGCGGGC 3

RESULT 667
ABZ95016
ID ABZ95016 standard; DNA; 10 BP.
XX
AC ABZ95016;

XX 17-OCT-2003 (first entry)
DT Human adenosine A1 receptor antisense fragment no.879.
XX
DE
DE
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 10258; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
| | | | |
Db 4 GGCGGGC 10

RESULT 668
ABX11772
ID ABX11772 standard; DNA; 10 BP.
XX
AC ABX11772;

XX 10-MAY-2003 (first entry)
DT Human K-RAS oncogene DNA nucleotides 138-147.
XX
DE
DE
KW Human; cancer; colon cancer; haematologic cancer; lung cancer;
KW prostate cancer; skin cancer; thyroid cancer; ovarian cancer;
KW K-RAS oncogene; K-RAS expression; cancer cell proliferation;
KW mutation-activated K-RAS expression; cytostatic; ds.
XX
OS Homo sapiens.
XX
PN US2002165196-A1.
XX
PD 07-NOV-2002.
XX
PF 07-MAY-2002; 2002US-00141263.
XX
PR 07-MAY-2001; 2001US-0289166P.
XX
PA (WICK/) WICKSTROM E.
XX
PI Wickstrom E;
XX
DR WPI; 2003-288145/28.
XX
PT Preventing or treating cancer, e.g. colon cancer, lung cancer or ovarian
PT cancer, comprises administering to a mammal an oligonucleotide targeted
PT to a nucleic acid encoding human K-RAS oncogene, and modulating K-RAS
PT expression.
XX
PS Disclosure; Page 10; 14pp; English.
XX
CC The present invention relates to a method for preventing or treating
CC cancers, such as colon, haematologic, lung, prostate, skin, thyroid, or
CC preferably ovarian cancer. The method comprises administering an
CC antisense oligonucleotide targeted to a nucleic acid encoding human K-RAS
CC oncogene, and modulating K-RAS expression. The oligonucleotides and
CC method of the invention inhibit cancer cell proliferation, and are useful
CC for preventing or treating cancers such as those mentioned above. The
CC oligonucleotides are also useful for research purposes, or for modulating
CC mutation-activated K-RAS expression in ovarian, colon, lung, thyroid,
CC prostate, skin, or haematologic cancer cells. The present sequence
CC represents human K-RAS oncogene DNA nucleotides 138-147 to which
CC antisense oligonucleotides can be targeted
XX
SQ Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7
| | | | |
Db 2 CGGCGGG 8

RESULT 669
ABX11773/C
ID ABX11773 standard; DNA; 10 BP.
XX
AC ABX11773;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human K-RAS oncogene antisense oligonucleotide KRAS8.
XX
KW Human; cancer; colon cancer; haematologic cancer; lung cancer;
KW prostate cancer; skin cancer; thyroid cancer; ovarian cancer;
KW K-RAS oncogene; K-RAS expression; cancer cell proliferation;
KW mutation-activated K-RAS expression; cytostatic; antisense; ss.
XX
OS Homo sapiens.

XX US2002165196-A1.
PN
XX
PD 07-NOV-2002.
XX
XX 07-MAY-2002; 2002US-00141263.
PF
XX 07-MAY-2001; 2001US-0289166P.
PR
XX (WICK/) WICKSTROM E.
PA
XX
XX Wickstrom E;
PI
XX WPI; 2003-288145/28.
DR
XX Preventing or treating cancer, e.g. colon cancer, lung cancer or ovarian
PT cancer, comprises administering to a mammal an oligonucleotide targeted
PT to a nucleic acid encoding human K-RAS oncogene, and modulating K-RAS
PT expression.
XX
PS Claim 19; Page 4; 14pp; English.
XX
CC The present invention relates to a method for preventing or treating
CC cancers, such as colon, haematologic, lung, prostate, skin, thyroid, or
CC preferably ovarian cancer. The method comprises administering an
CC antisense oligonucleotide targeted to a nucleic acid encoding human K-RAS
CC oncogene, and modulating K-RAS expression. The oligonucleotides and
CC method of the invention inhibit cancer cell proliferation, and are useful
CC for preventing or treating cancers such as those mentioned above. The
CC oligonucleotides are also useful for research purposes, or for modulating
CC mutation-activated K-RAS expression in ovarian, colon, lung, thyroid,
CC prostate, skin, or haematologic cancer cells. The present sequence
CC represents an antisense oligonucleotide of the invention
XX
SQ Sequence 10 BP; 0 A; 7 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7
Db 9 CGGCGGG 3

RESULT 670
ADM22167
ID ADM22167 standard; DNA; 10 BP.
XX
AC ADM22167;
XX
DT 20-MAY-2004 (first entry)
XX
DE Synthetic zinc finger protein target DNA #433.
XX
KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX
OS Unidentified.
XX
XX US2003104526-A1.
PN
XX
PD 05-JUN-2003.
XX
PF 20-NOV-2001; 2001US-00989994.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI
XX
XX WPI; 2003-843091/78.
DR
XX New zinc finger protein used for recognizing triplet target subsites
PT having nucleotide G in 5'-most position of subsite, that has been
PT optimized with respect to location of subsite within target site.
PT
XX
PS Example 6; SEQ ID NO 1641; 48pp; English.
XX
CC The invention describes a new zinc finger protein that binds to a target
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC (S3) target subsites. The zinc finger proteins can be used for
CC recognising triplet target subsites having the nucleotide G in the 5' -
CC most position of the subsite, that has been optimised with respect to the
CC location of the subsite within the target site. This sequence represents
CC the target polynucleotide of a synthetic zinc finger protein of the
CC invention.

XX Liu Q;
PI
XX WPI; 2003-843091/78.
DR
XX New zinc finger protein used for recognizing triplet target subsites
PT having nucleotide G in 5'-most position of subsite, that has been
PT optimized with respect to location of subsite within target site.
PT
XX
PS Example 6; SEQ ID NO 1640; 48pp; English.
XX
CC The invention describes a new zinc finger protein that binds to a target
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC (S3) target subsites. The zinc finger proteins can be used for
CC recognising triplet target subsites having the nucleotide G in the 5' -
CC most position of the subsite, that has been optimised with respect to the
CC location of the subsite within the target site. This sequence represents
CC the target polynucleotide of a synthetic zinc finger protein of the
CC invention.

XX SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGGGCA 12
Db 3 GCGGGCA 9

RESULT 671
ADM22168
ID ADM22168 standard; DNA; 10 BP.
XX
AC ADM22168;
XX
DT 20-MAY-2004 (first entry)
XX
DE Synthetic zinc finger protein target DNA #434.
XX
KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX
OS Unidentified.
XX
XX US2003104526-A1.
PN
XX
PD 05-JUN-2003.
XX
PF 20-NOV-2001; 2001US-00989994.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
XX
PI Liu Q;
XX
XX WPI; 2003-843091/78.
DR
XX New zinc finger protein used for recognizing triplet target subsites
PT having nucleotide G in 5'-most position of subsite, that has been
PT optimized with respect to location of subsite within target site.
PT
XX
PS Example 6; SEQ ID NO 1641; 48pp; English.
XX
CC The invention describes a new zinc finger protein that binds to a target

CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC (S3) target subsites. The zinc finger proteins can be used for
CC recognising triplet target subsites having the nucleotide G in the 5'-
CC most position of the subsite, that has been optimised with respect to the
CC location of the subsite within the target site. This sequence represents
CC the target polynucleotide of a synthetic zinc finger protein of the
CC invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
Db 3 GGCGGCA 9

RESULT 672
ADM29239
ID ADM29239 standard; DNA; 10 BP.
XX
AC ADM29239;
XX
DT 20-MAY-2004 (first entry)
XX
DE NotI site for cDNA cloning.
XX
KW NotI; ss; intestinal trefoil factor; pancreatic spasmolytic peptide; PSP;
KW pS2; antiinflammatory; ophthalmological; antibacterial; antiemetic;
KW cytostatic; immunosuppressive; tranquiliser; vulnerary; antiapoptotic;
KW eye epithelium; microbial infection; viral infection;
KW bacterial infection; fungal infection; adenoviral infection;
KW herpes simplex virus infection; eye disease; corneal ulcer;
KW ocular inflammatory disease; corneal epithelial wound healing;
KW digestive tract disorder; gastritis; ulcer; gastric cancer;
KW MALT lymphoma; Menetrier's disease; inflammatory bowel disease.
XX
OS Synthetic.
XX
PN US2003134797-A1.
XX
PD 17-JUL-2003.
XX
PF 06-DEC-2002; 2002US-00313642.
XX
PR 17-MAY-1999; 99US-00313434.
XX
PA (PODO/) PODOLSKY D K.
XX
PI Podolsky DK;
XX
DR WPI; 2003-897264/82.
XX
PT Treating disruption of epithelium of patient's eye comprises
PT administering trefoil protein, e.g. intestinal trefoil factor to
PT patient's eye.
XX
PS Example 3; SEQ ID NO 5; 33pp; English.
XX
CC The invention relates to treating the disruption of the epithelium of the
CC eye in a patient comprising administering a trefoil protein to the eye of
CC the patient. The trefoil protein is intestinal trefoil factor (ITF),
CC pancreatic spasmolytic peptide (PSP), pS2 or their biologically active
CC fragments. The disruption is caused by microbial infection (viral,
CC bacterial, or fungal infection). The viral infection is adenoviral
CC infection or herpes simplex virus infection. The trefoil proteins of the
CC invention are resistant to destruction in the digestive tract and
CC effectively treat eye diseases (e.g. corneal ulcer, ocular inflammatory
CC disease) and have the ability to enhance corneal epithelial wound

CC healing. The proteins are also useful in treating digestive tract
CC disorders e.g. gastritis, ulcers, gastric cancer, MALT lymphoma,
CC Menetrier's disease and inflammatory bowel disease. The present sequence
CC is a NotI site which may be engineered onto isolated cDNA to facilitate
CC cloning.
XX
SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCGGGC 11
Db 1 GGCGGGC 7

RESULT 673
ABD18875
ID ABD18875 standard; DNA; 10 BP.
XX
AC ABD18875;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human adenosine A1 receptor oligonucleotide fragment 890.
XX
KW Human; antisenese; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 10269; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCGGGC 8
Db 3 GGCGGGC 9

RESULT 674

ABD18885
ID ABD18885 standard; DNA; 10 BP.

XX
AC ABD18885;

DT 29-JUL-2004 (first entry)

XX Human adenosine A1 receptor oligonucleotide fragment 900.

DE
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.

XX Homo sapiens.

OS
XX WO200285309-A2.

PN
XX 31-OCT-2002.

PD
XX 23-APR-2002; 2002WO-US013143.

PF
XX 24-APR-2001; 2001US-0286036P.

PR
XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

DR
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 10279; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,

CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCGGGC 8
Db 2 GGCGGGC 8

RESULT 675

ABD18864

ID ABD18864 standard; DNA; 10 BP.

XX
AC ABD18864;

XX 29-JUL-2004 (first entry)

DE Human adenosine A1 receptor oligonucleotide fragment 879.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
DR
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 10258; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
Db |||||
4 GCGGGGC 10

RESULT 676
ABD18967/c
ID ABD18967 standard; DNA; 10 BP.
XX
AC ABD18967;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human adenosine A2b receptor oligonucleotide fragment 1674.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ds.
OS Homo sapiens.

XX WO200285309-A2.
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002WO-US013143.
PF
XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
DR
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 11058; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9
Db |||||
9 GCGGGCG 3

RESULT 677
ABD18894
ID ABD18894 standard; DNA; 10 BP.
XX
AC ABD18894;
XX
DT 29-JUL-2004 (first entry)
XX

DE Human adenosine A1 receptor oligonucleotide fragment 909.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;

KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;

KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;

KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;

KW pulmonary transplantation rejection; ds.

XX Homo sapiens.

OS

XX WO200285309-A2.

PN

XX

PD 31-OCT-2002.

XX

XX 23-APR-2002; 2002WO-US013143.

PF

XX 24-APR-2001; 2001US-0286036P.

PR

XX (EPIG-) EPIGENESIS PHARM INC.

PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

PI

XX WPI; 2003-093058/08.

DR

XX Pharmaceutical composition for treating asthma, has antisense

XX oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

PT

XX Claim 15; SEQ ID NO 10288; 763pp; English.

PS

XX This invention describes a novel composition (a) a first active agent,

CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)

CC instructions for adding a carrier and for use of the kit. The composition

CC of the invention has antiallergic, antiinflammatory, antiasthmatic,

CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or

CC treating a respiratory, lung or malignant disease. The administered

CC composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to

CC reduce the amount of target polypeptide present in the lungs. The

CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated

CC with a disease or condition such as pulmonary vasoconstriction,

CC inflammation, allergies, asthma, impeded respiration, respiratory

CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

CC transplantation rejection, pulmonary infections, bronchitis or cancer.

CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of

CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

CC prevent any unwanted effects due to it

XX

SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGCGC 8

Db 1 GGCGGCGC 7

RESULT 678

ADH57613/c

ID ADH57613 standard; DNA; 10 BP.

XX

AC ADH57613;

XX

DT 25-MAR-2004 (first entry)

XX

DE Extendable oligo E102 for DNA sequencing and PCR amplification.

XX

KW ss; primer library; extendable oligo; EO; ligation chain reaction; LCR;

KW rolling circle amplification; strand displacement amplification;

KW isothermal DNA amplification; biotechnology; agriculture;

KW medical research; 2,4 diaminopurine nucleotide analogue; PCR; primer.

XX

OS Synthetic.

XX WO2003093500-A1.

PN

XX 13-NOV-2003.

PD

XX 24-DEC-2002; 2002WO-AU001763.

PF

XX 01-MAY-2002; 2002AU-00002045.

PR

XX (NUCL-) NUCLEICS PTY LTD.

PA

XX Tillet D, Thomas T;

PI

XX WPI; 2004-053046/05.

DR

XX Increasing the affinity of an extendable oligonucleotide (EO) for a

PT target nucleic acid, for providing primers having improved specificity,

PT comprises hybridization of the EO to a template oligonucleotide (TO) and

PT extension of the EO.

XX

PS Example 9; Page 41; 85pp; English.

XX

CC This invention relates to a novel method for the optimisation of primer

CC libraries. Specifically, it refers to increasing the affinity of short

CC oligonucleotide primers, also known as extendable oligos (EOs), for their

CC template sequences. The present invention describes improved methods for

CC sequencing and the linear and exponential amplification of DNA that can

CC be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle

CC amplification, strand displacement amplification and isothermal DNA

CC amplification. Accordingly, these extendable oligos with improved

CC specificity and affinity are particularly important in fields ranging

CC from biotechnology and agriculture to medical research. This

CC oligonucleotide sequence is an extendable oligonucleotide that includes

CC an adenine replacement 2,4 diaminopurine nucleotide analogue in the catch

CC region, and is useful for both DNA sequencing reactions and PCR

CC amplification in an exemplification of the invention.

XX

SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCGGCGG 10

Db 10 GGCGGCGG 4

RESULT 679

ADH57601/c

ID ADH57601 standard; DNA; 10 BP.

XX

AC ADH57601;

XX 25-MAR-2004 (first entry)
XX Extendable oligo E090 for DNA sequencing and PCR amplification.
DE ss; primer library; extendable oligo; EO; ligation chain reaction; LCR;
XX rolling circle amplification; strand displacement amplification;
KW isothermal DNA amplification; biotechnology; agriculture;
KW medical research; 2,4 diaminopurine nucleotide analogue; PCR; primer.
XX Synthetic.
OS WO2003093500-A1.
XX 13-NOV-2003.
XX 24-DEC-2002; 2002WO-AU001763.
XX 01-MAY-2002; 2002AU-00002045.
XX (NUCL-) NUCLEICS PTY LTD.
PA Tillett D, Thomas T;
XX WPI; 2004-053046/05.
DR Increasing the affinity of an extendable oligonucleotide (EO) for a
XX target nucleic acid, for providing primers having improved specificity,
PT comprises hybridization of the EO to a template oligonucleotide (TO) and
PT extension of the EO.
XX Example 9; Page 40; 85pp; English.
PS This invention relates to a novel method for the optimisation of primer
XX libraries. Specifically, it refers to increasing the affinity of short
CC oligonucleotide primers, also known as extendable oligos (EOs), for their
CC template sequences. The present invention describes improved methods for
CC sequencing and the linear and exponential amplification of DNA that can
CC be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle
CC amplification, strand displacement amplification and isothermal DNA
CC amplification. Accordingly, these extendable oligos with improved
CC specificity and affinity are particularly important in fields ranging
CC from biotechnology and agriculture to medical research. This
CC oligonucleotide sequence is an extendable oligonucleotide that includes
CC an adenine replacement 2,4 diaminopurine nucleotide analogue in the catch
CC region, and is useful for both DNA sequencing reactions and PCR
CC amplification in an exemplification of the invention.
XX Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
SQ Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGCGG 7
Db 10 CGCGCGG 4
RESULT 680
ADS76874
ID ADS76874 standard; DNA; 10 BP.
XX ADS76874;
AC 30-DEC-2004 (first entry)
XX Breast cancer detection oligonucleotide #656.
DE ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW

KW collagen antagonist; diagnosis; breast tissue; cancer.
XX Homo sapiens.
XX WO2004085621-A2.
XX 07-OCT-2004.
XX 22-MAR-2004; 2004WO-US008866.
XX 20-MAR-2003; 2003US-0456735P.
XX (DAND) DANA FARBER CANCER INST INC.
PA Polyak K, Porter D, Allinen M;
XX WPI; 2004-728732/71.
DR Diagnosing breast cancer comprises determining expression levels of a
XX gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX Example 2; SEQ ID NO 656; 149pp; English.
PS The invention relates to a method of diagnosis (M1) comprising: (a)
XX providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
SQ Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGCGGGC 8
Db 3 GGCGGGC 9
RESULT 681
ADS77539/c
ID ADS77539 standard; DNA; 10 BP.
XX ADS77539;
AC 30-DEC-2004 (first entry)
XX Breast cancer detection oligonucleotide #1321.
DE ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX Homo sapiens.
OS WO2004085621-A2.
XX 07-OCT-2004.
XX 22-MAR-2004; 2004WO-US008866.
XX 20-MAR-2003; 2003US-0456735P.
XX (DAND) DANA FARBER CANCER INST INC.

XX Polyak K, Porter D, Allinen M;
XX WPI; 2004-728732/71.
XX Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
XX Example 6; SEQ ID NO 1321; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
Db 7 GGGCGGC 1

RESULT 682
ADS77304/C
ID ADS77304 standard; DNA; 10 BP.
XX
AC ADS77304;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #1086.
XX
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
DR WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
XX Example 2; SEQ ID NO 1086; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)

CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
Db 7 GGGCGGC 1

RESULT 683
ADS77303/C
ID ADS77303 standard; DNA; 10 BP.
XX
AC ADS77303;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #1085.
XX
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
DR WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
PS Example 2; SEQ ID NO 1085; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

XX 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND) DANA FARBER CANCER INST INC.
XX PA Polyak K, Porter D, Allinen M;
XX PI WPI; 2004-728732/71.
XX
DR
XX
PT Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
PS Example 2; SEQ ID NO 581; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;
XX
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCGGG 7
Db 8 CGGCGGG 2
RESULT 687
ADS76873
ID ADS76873 standard; DNA; 10 BP.
XX
AC ADS76873;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #655.
XX
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
XX Polyak K, Porter D, Allinen M;
XX
DR WPI; 2004-728732/71.
XX

PT Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
PS Example 2; SEQ ID NO 655; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
XX
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GCGCGGC 8
Db 3 GCGCGGC 9
RESULT 688
ADS76366/c
ID ADS76366 standard; DNA; 10 BP.
XX
AC ADS76366;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #148.
XX
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
XX Polyak K, Porter D, Allinen M;
XX
DR WPI; 2004-728732/71.
XX
PT Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
PS Example 2; SEQ ID NO 148; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the

CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.

XX
SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7
Db 8 CGGCGGG 2

RESULT 689
ADU18811
ID ADU18811 standard; DNA; 10 BP.
XX
AC ADU18811;
XX
DT 13-JAN-2005 (first entry)
XX
DE Hypoxia-related tumourigenesis-related SAGE tag #602.
XX
KW screening; hypoxia-related tumourigenesis;
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX
OS Unidentified.
XX
PN WO2004092198-A2.
XX
PD 28-OCT-2004.
XX
PF 09-APR-2004; 2004WO-US011087.
XX
PR 09-APR-2003; 2003US-0461712P.
XX
PA (GENZ) GENZYME CORP.
XX
PI Nacht M;
XX
DR WPI; 2004-758333/74.
XX

PT Identifying agents that alter biological activity of a polypeptide
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
PT comprises contacting an agent with a target cell and monitoring activity
PT of expressed product.

XX
PS Disclosure; Page 67; 100pp; English.
XX
CC The invention comprises a method of screening for candidate agents
CC capable of altering the biological activity of a protein encoded by a
CC nucleotide involved in hypoxia-related tumourigenesis. The method of the
CC invention involves: contacting a test agent with a target cell expressing
CC the nucleotide, and monitoring the activity of the expressed protein
CC product; if the test agent modifies the activity of the expressed protein
CC then this is a candidate agent. The method of the invention is useful for
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
CC or treating tumours. The present DNA sequence represents a SAGE tag that
CC was used in the exemplification of the invention.

XX
SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db 4 GGGCGGC 10

RESULT 690
ADW10555
ID ADW10555 standard; DNA; 10 BP.
XX
AC ADW10555;
XX
DT 24-MAR-2005 (first entry)
XX
DE Human genomic DNA fragment arbitrarily-primed PCR primer, GC5.
XX
KW colorectal tumor; CpG methylation detection; cytostatic; gene therapy;
KW proliferative disorder; carcinoma; PCR; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2004265833-A1.
XX
PD 30-DEC-2004.
XX
PF 23-JUN-2003; 2003US-00602494.
XX
PR 23-JUN-2003; 2003US-00602494.
XX
PA (LOFT/) LOFTON-DAY C.
PA (SLED/) SLEDZIEWSKI A.
PA (THOM/) THOMAS J.
PA (DAYR/) DAY R W.
PA (TONN/) TONNES-PRIDDY L.
PA (CARD/) CARDON K.
XX

Lofton-Day C, Sledziewski A, Thomas J, Day RW, Tonnes-Priddy L;
Cardon K;

WPI; 2005-089566/10.

Detecting and distinguishing colorectal cell proliferative disorders by
contacting genomic DNA of biological sample with reagent that
distinguishes methylated and non-methylated CpG dinucleotides within
target sequence of genomic DNA.

Example 1; SEQ ID NO 360; 23pp; English.

The invention relates to a novel method for detecting and distinguishing
between, or among, colorectal cell proliferative disorders. The method
involves contacting genomic DNA of a biological sample obtained from the
subject with one or more reagent(s), or a series of reagents that
distinguishes between methylated and non-methylated CpG dinucleotides
within a target sequence of the genomic DNA. The invention further
comprises: a nucleic acid comprising a sequence of 18 or more contiguous
nucleotides of a treated genomic DNA sequence chosen from any one of 284
fully defined nucleotide sequences, whose sequence listing is not
provided in the specification, and their complementary sequences, where
the contiguous sequence has one or more CpG, TpA, or CpA dinucleotide,
and the treatment is suitable to convert one or more of the unmethylated
cytosine base(s) of the genomic DNA sequence initially to uracil or
another base that is detectably dissimilar to cytosine in terms of
hybridization; an oligomer or peptide nucleic acid (PNA)-oligomer,
comprising 9 or more contiguous nucleotides that is complementary to or
hybridizes under moderately stringent or stringent conditions to one of
the 284 DNA sequences and their complementary sequences provided in the
source document, which is treated; a set of oligomers comprising two or
more of the oligomer of PNA-oligomer; an array of oligomers; and a kit
for carrying out the above methods. The method and its novel compositions
have cytostatic activity. The polynucleotide sequence may be used in gene
therapy. The above methods are useful for detecting and distinguishing
between, or among, colorectal cell proliferative disorders chosen from
colorectal carcinoma, colon adenomas and colon polyps, in a biological
sample, such as histological slides, biopsies, paraffin embedded tissue,
bodily fluids, stool, blood, serum, plasma and their combinations. The
oligomer array is useful as a probe for detecting one or more of the
cytosine methylation state, or single nucleotide polymorphisms within the
genomic DNA or their complementary sequences. The polynucleotides of the

CC invention are useful for classifying, distinguishing between, or among,
CC diagnosing or determining the predisposition for colorectal cell
CC proliferative disorders, or for the therapy of colorectal cell
CC proliferative disorders. This polynucleotide sequence represents a primer
CC used in the exemplification of the invention.

XX
SQ Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||||||
Db 4 GGGCGGC 10

RESULT 691
ADZ67948
ID ADZ67948 standard; DNA; 10 BP.

XX
AC ADZ67948;

XX
DT 14-JUL-2005 (first entry)

XX
DE NTRK1 gene polymorphic site 12 primer extension oligonucleotide.

XX
KW Neurotrophic tyrosine kinase receptor type 1; NTRK1; Alzheimers disease;
KW neurological disease; diagnosis; prognosis; primer; SNP detection;
KW haplotype mapping; ss.

XX
OS Homo sapiens.

XX
PN WO2005037204-A2.

XX
PD 28-APR-2005.

XX
PF 14-OCT-2004; 2004WO-US033689.

XX
PR 15-OCT-2003; 2003US-0511247P.

XX
PA (GENA-) GENAISSANCE PHARM.

XX
PI Aerssens J, Athanasiou M, Brain C, Cohen N, Dain B, Denton RR;
PI Judson RS, Ozdemir V, Reed CR;

XX
DR WPI; 2005-322749/33.

XX
PT Determining whether individual has age of onset marker I or marker II, by
PT determining whether individual has zero copies or copy of neurotrophic
PT tyrosine kinase, receptor, type 1 haplotypes involved in onset of
PT Alzheimer's disease.

XX
PS Disclosure; SEQ ID NO 46; 128pp; English.

XX
CC The inventors have discovered a set of 112 haplotypes in the human
CC neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) gene ADZ67903 that
CC are associated with the age of onset of Alzheimer's disease (AD). They
CC have also discovered that the copy number of each of these NTRK1
CC haplotypes affects the age of onset of AD. If an individual has at least
CC one copy of any of the 112 specified haplotypes, that individual is
CC defined as having an 'age of onset marker I' and is more likely to have a
CC later age of onset of AD than an individual having zero copies of any of
CC the 112 haplotypes, such an individual being defined as 'age of onset
CC marker II'. Testing for the presence or absence, and copy number, of the
CC haplotypes is useful for predicting the age at which individuals who are
CC at increased risk of AD are likely to develop AD and to help confirm a
CC diagnosis of mild or minimal cognitive impairment (MDI) or AD. Such
CC knowledge will assist therapy and lifestyle decisions. The correlation of
CC certain NTRK1 haplotypes with age of AD onset indicates that variation in
CC the NTRK1 gene should be considered in the development and clinical
CC trials of drugs for treating MCI, AD and other neurodegenerative
CC disorders. This correlation also provides a basis for pursuing NTRK1 as a

CC target for drugs designed to treat cognitive disorders such as MDI, AD
CC and other neurological diseases or conditions. Information is provided
CC about the composition of each of 112 haplotypes, namely the location in
CC the NTRK1 gene of each of the polymorphic sites (PSs) and the identity of
CC the reference and variant allele at each PS. An individual's genotype for
CC the set of PSs is obtained by primer extension, mismatch detection, enzymatic
CC nucleic acid amplification, hybridization, mismatch detection, enzymatic
CC nucleic acid cleavage or sequencing assay. The present sequence is that
CC of a reverse primer extension oligonucleotide for detecting PS12 in
CC haplotypes comprising preferred embodiments of age of onset markers I and
CC II.

XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGCGG 10
|||||||
Db 2 CGGCGG 8

RESULT 692
AEA62015
ID AEA62015 standard; DNA; 10 BP.

XX
AC AEA62015;

XX
DT 11-AUG-2005 (first entry)

XX
DE NTRK1 gene polymorphic site 12 primer extension oligonucleotide.

XX
KW NTRK1 gene; neurotrophic tyrosine kinase, receptor, type 1;
KW Alzheimers disease; degeneration; neurological disease;
KW haplotype mapping; prognosis; primer; ss; SNP detection.

OS
Homo sapiens.

XX
PN WO2005052180-A2.

XX
PD 09-JUN-2005.

XX
PF 22-NOV-2004; 2004WO-US038876.

XX
PR 24-NOV-2003; 2003US-0524636P.

XX
PA (GENA-) GENAISSANCE PHARM INC.

XX
PI Aerssens J, Athanasiou M, Brain C, Cohen N, Dain B, Denton RR;
PI Judson RS, Ozdemir V, Reed CR;

XX
DR WPI; 2005-418015/42.

XX
PT Determining whether an individual has a progression marker I or
PT progression marker II, useful for predicting an individual's progression
PT of Alzheimer's disease, by determining whether the individual has any of
PT the NTRK1 haplotypes.

PS
Claim 40; SEQ ID NO 56; 108pp; English.

XX
CC The present invention relates to genetic markers of the human
CC neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) gene AEA61960 that
CC are associated with progression of Alzheimer's disease (AD). 12
CC Polymorphic sites (PSs) have been discovered in the NTRK1 gene of
CC Caucasian individuals with AD, and a set of 70 haplotypes having
CC association with progression of AD have been identified. If an individual
CC has 0 or 1 copy of any of haplotypes 1-41 and 67-70, or 0 copies of any
CC of haplotypes 42-66, then that individual is defined as having a
CC progression marker I and is more likely to exhibit a slower progression
CC of AD than an individual having 2 copies of any of haplotypes 1-41 and 67
CC -70, or at least 1 copy of any of haplotypes 42-66, such an individual
CC being defined as having a progression marker II. Additional haplotypes

CC may be identified that are in linkage disequilibrium with any of
CC haplotypes 1-70, referred to as linked haplotypes and substitute
CC haplotypes of any of haplotypes 1-70, in which one or more of the PSs in
CC the original haplotype is substituted with another PS, where the allele
CC at the substituted PS is in linkage disequilibrium with the allele at the
CC substituting PS. The invention provides methods and kits for determining
CC whether an individual has a progression marker I or a progression marker
CC II. A method is also provided for predicting an individual's progression
CC of AD. The individual is especially a Caucasian diagnosed as having a
CC cognitive disorder. An individual's genotype for each PS may be obtained
CC by primer extension, allele-specific PCR, nucleic acid amplification,
CC hybridization, mismatch-detection, enzymatic nucleic acid cleavage or
CC sequencing assay. The present sequence is a reverse primer extension
CC oligonucleotide that can be used to detect the allele at PS12 of the
CC NTRK1 gene. The 3' terminus of the oligonucleotide is complementary to
CC the nucleotide located immediately adjacent to the PS. The
CC oligonucleotide is included in a claimed kit of the invention used to
CC determine whether an individual has a progression marker I or progression
CC marker II.
XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGG 10
|||
Db 2 CGGGCGG 8

RESULT 693
AEA52329
ID AEA52329 standard; DNA; 10 BP.
XX
AC AEA52329;
XX
DT 25-AUG-2005 (first entry)
XX
DE Prostate cancer gene PCR primer SEQ ID NO 932.
XX
KW gene expression; cell proliferation; hyperproliferation; cytostatic;
KW neoplasm; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2005054517-A2.
XX
PD 16-JUN-2005.
XX
PF 01-DEC-2004; 2004WO-US040289.
XX
PR 01-DEC-2003; 2003EP-00090414.
PR 10-FEB-2004; 2004EP-00090040.
PR 10-MAY-2004; 2004EP-00090187.
PR 21-JUL-2004; 2004EP-00090292.
XX
PA (EPIG-) EPIGENOMICS AG.
XX

Day KJ, Cottrell S, Distler J, Morotti A, Yamamura S, Dekker S;
Pi Ocamp Y, Devos T;
XX
DR WPI; 2005-425434/43.
XX
PT Detecting and/or differentiating prostate cell proliferative disorders in
PT a subject by contacting genomic with reagent(s) that distinguishes
PT between methylated and non-methylated CpG dinucleotides in target nucleic
PT acids.
XX
PS Example 1; SEQ ID NO 932; 164pp; English.
XX
CC The invention describes a method of detecting and/or differentiating
CC between prostate cell proliferative disorders in a subject comprising

CC contacting genomic DNA isolated from a biological sample with at least
CC one reagent, or series of reagents that distinguishes between methylated
CC and non-methylated CpG dinucleotides within one or a combination of
CC target nucleic acids e.g. HISTONE H4. Also described are: a treated
CC nucleic acid derived from SEQ ID NO: 1-59, 1017-1028, 1116, 1171, where
CC the treatment converts at least one unmethylated cytosine base of the
CC genomic DNA sequence to uracil or another base that is detectable
CC dissimilar to cytosine in terms of hybridization; a nucleic acid
CC comprising at least 16 contiguous nucleotides of a treated genomic DNA
CC sequence selected from SEQ ID NO: 60-295, 1029-1076, 1117-1120, 1172-1175
CC and sequences complementary to them; an oligomer comprising a sequence of
CC at least 9 contiguous nucleotides that is complementary to, or hybridizes
CC under moderately stringent or stringent conditions to a treated genomic
CC DNA sequence above; a set of oligomers comprising at least two
CC oligonucleotides as above; and a kit useful for detecting and/or
CC distinguishing between or among prostate cell proliferative disorder of a
CC subject comprising at least one of a bisulfite reagent, or a methylation-
CC sensitive restriction enzyme, and at least one nucleic acid molecule or
CC peptide nucleic acid molecule comprising a contiguous sequence at least 9
CC nucleotides that is complementary to, or hybridizes under moderately
CC stringent or stringent conditions to a sequence selected from SEQ ID NO:
CC 60-295, 1029-1076, 1117-1120, 1172-1175 and their complements. The
CC method, nucleic acid, oligomer, set of oligonucleotide, and kit are
CC useful for detecting and/or differentiating between or among cell
CC proliferative disorders. This sequence represents a primer used to
CC analyze methylation status of genes encoding a prostate cell
CC proliferation associated protein.
XX

SQ Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||
Db 4 GGGCGGC 10

Search completed: May 9, 2006, 16:45:22
Job time : 1 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:47:24 ; Search time 1 Seconds
(without alignments)
0.075 Million cell updates/sec

Title: US-09-904-968A-20-COPY
Perfect score: 16
Sequence: 1 cggcgggcggcatcgt 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 210 seqs, 2342 residues

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 211 summaries

Database : pubmaindb20:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	16	1	US-09-904-968A-20
2	12.4	77.5	14	1	US-10-291-230-19
3	12.4	77.5	14	1	US-10-291-249-19
4	11.4	71.2	16	1	US-10-712-672-1460
5	11.4	71.2	16	1	US-10-712-672-1461
6	10.8	67.5	14	1	US-09-093-972C-695
7	10.8	67.5	14	1	US-10-758-451-695
8	10.8	67.5	15	1	US-09-093-972C-673
9	10.8	67.5	15	1	US-09-093-972C-694
10	10.8	67.5	15	1	US-10-758-451-673
11	10.8	67.5	15	1	US-10-758-451-694
12	10.4	65.0	12	1	US-09-093-972C-697
13	10.4	65.0	12	1	US-10-758-451-697
14	10.4	65.0	13	1	US-09-093-972C-675
15	10.4	65.0	13	1	US-09-093-972C-696
16	10.4	65.0	13	1	US-10-758-451-675
17	10.4	65.0	13	1	US-10-758-451-696
18	10.4	65.0	14	1	US-09-093-972C-652
19	10.4	65.0	14	1	US-09-093-972C-674
20	10.4	65.0	14	1	US-10-758-451-652
21	10.4	65.0	14	1	US-10-758-451-674
22	10	62.5	10	1	US-10-487-934-312
23	10	62.5	13	1	US-10-091-281-458
24	10	62.5	13	1	US-10-257-017B-100005
25	10	62.5	13	1	US-10-257-017B-100006
26	10	62.5	13	1	US-10-257-017B-229445
27	10	62.5	13	1	US-10-257-017B-229446
28	10	62.5	13	1	US-10-257-017B-229447
29	10	62.5	13	1	US-10-257-017B-229448
30	9.8	61.2	13	1	US-09-093-972C-716
31	9.8	61.2	13	1	US-10-758-451-716
32	9.8	61.3	14	1	US-09-504-231A-1425
33	9.8	61.3	14	1	US-09-274-553D-1425
					Sequence 20, Appl
					Sequence 19, Appl
					Sequence 19, Appl
					Sequence 1460, Ap
					Sequence 1461, Ap
					Sequence 695, App
					Sequence 695, App
					Sequence 673, App
					Sequence 694, App
					Sequence 673, App
					Sequence 694, App
					Sequence 697, App
					Sequence 675, App
					Sequence 696, App
					Sequence 675, App
					Sequence 696, App
					Sequence 652, App
					Sequence 674, App
					Sequence 652, App
					Sequence 674, App
					Sequence 312, App
					Sequence 458, App
					Sequence 100005,
					Sequence 100006,
					Sequence 229445,
					Sequence 229446,
					Sequence 229447,
					Sequence 229448,
					Sequence 716, App
					Sequence 716, App
					Sequence 1425, Ap
					Sequence 1425, Ap

34	9.8	61.2	14	1	US-09-093-972C-715	Sequence 715, App
35	9.8	61.2	14	1	US-10-758-451-715	Sequence 715, App
36	9.4	58.7	11	1	US-09-093-972C-698	Sequence 698, App
37	9.4	58.7	11	1	US-09-093-972C-718	Sequence 718, App
38	9.4	58.7	11	1	US-09-093-972C-755	Sequence 755, App
39	9.4	58.7	11	1	US-10-758-451-698	Sequence 698, App
40	9.4	58.7	11	1	US-10-758-451-718	Sequence 718, App
41	9.4	58.7	11	1	US-10-758-451-755	Sequence 755, App
42	9.4	58.7	12	1	US-09-093-972C-676	Sequence 676, App
43	9.4	58.7	12	1	US-09-093-972C-717	Sequence 717, App
44	9.4	58.7	12	1	US-09-093-972C-736	Sequence 736, App
45	9.4	58.7	12	1	US-09-093-972C-754	Sequence 754, App
46	9.4	58.7	12	1	US-10-758-451-676	Sequence 676, App
47	9.4	58.7	12	1	US-10-758-451-717	Sequence 717, App
48	9.4	58.7	12	1	US-10-758-451-736	Sequence 736, App
49	9.4	58.7	12	1	US-10-758-451-754	Sequence 754, App
50	9.4	58.7	13	1	US-09-093-972C-653	Sequence 653, App
51	9.4	58.7	13	1	US-09-093-972C-735	Sequence 735, App
52	9.4	58.7	13	1	US-09-093-972C-753	Sequence 753, App
53	9.4	58.7	13	1	US-10-257-017B-227179	Sequence 227179,
54	9.4	58.7	13	1	US-10-257-017B-227180	Sequence 227180,
55	9.4	58.7	13	1	US-10-758-451-653	Sequence 653, App
56	9.4	58.7	13	1	US-10-758-451-735	Sequence 735, App
57	9.4	58.7	13	1	US-10-758-451-753	Sequence 753, App
58	9	56.2	10	1	US-09-093-972C-738	Sequence 738, App
59	9	56.2	10	1	US-09-093-972C-756	Sequence 756, App
60	9	56.2	10	1	US-10-758-451-738	Sequence 738, App
61	9	56.2	10	1	US-10-758-451-756	Sequence 756, App
62	9	56.2	11	1	US-09-093-972C-737	Sequence 737, App
63	9	56.2	11	1	US-10-758-451-737	Sequence 737, App
64	9	56.2	12	1	US-09-739-068-13	Sequence 13, Appl
65	9	56.2	12	1	US-10-091-281-459	Sequence 459, App
66	9	56.2	12	1	US-10-257-017B-269661	Sequence 269661,
67	9	56.2	12	1	US-10-257-017B-289845	Sequence 289845,
68	9	56.2	12	1	US-10-257-017B-322850	Sequence 322850,
69	9	56.2	12	1	US-10-257-017B-322854	Sequence 322854,
70	9	56.2	12	1	US-10-257-017B-322858	Sequence 322858,
71	9	56.2	12	1	US-10-257-017B-322859	Sequence 322859,
72	8.8	55.0	12	1	US-10-257-017B-299697	Sequence 299697,
73	8.8	55.0	12	1	US-10-257-017B-311797	Sequence 311797,
74	8.4	52.5	10	1	US-09-093-972C-699	Sequence 699, App
75	8.4	52.5	10	1	US-09-093-972C-719	Sequence 719, App
76	8.4	52.5	10	1	US-09-093-972C-773	Sequence 773, App
77	8.4	52.5	10	1	US-10-113-877-39	Sequence 39, Appl
78	8.4	52.5	10	1	US-10-146-354A-4	Sequence 4, Appli
79	8.4	52.5	10	1	US-10-356-792-27	Sequence 27, Appl
80	8.4	52.5	10	1	US-10-602-494-366	Sequence 366, App
81	8.4	52.5	10	1	US-10-758-451-699	Sequence 699, App
82	8.4	52.5	10	1	US-10-758-451-719	Sequence 719, App
83	8.4	52.5	10	1	US-10-758-451-773	Sequence 773, App
84	8.4	52.5	11	1	US-08-944-410-79	Sequence 79, Appl
85	8.4	52.5	11	1	US-09-974-143A-10	Sequence 10, Appl
86	8.4	52.5	11	1	US-09-093-972C-677	Sequence 677, App
87	8.4	52.5	11	1	US-09-093-972C-772	Sequence 772, App
88	8.4	52.5	11	1	US-10-112-267-44	Sequence 44, Appl
89	8.4	52.5	11	1	US-10-214-417A-45	Sequence 45, Appl
90	8.4	52.5	11	1	US-10-434-588-41	Sequence 41, Appl
91	8.4	52.5	11	1	US-10-628-770-24	Sequence 24, Appl
92	8.4	52.5	11	1	US-10-762-154-32	Sequence 32, Appl
93	8.4	52.5	11	1	US-10-659-549-23	Sequence 23, Appl
94	8.4	52.5	11	1	US-10-758-451-677	Sequence 677, App
95	8.4	52.5	11	1	US-10-758-451-772	Sequence 772, App
96	8.4	52.5	12	1	US-09-093-972C-654	Sequence 654, App
97	8.4	52.5	12	1	US-09-093-972C-771	Sequence 771, App
98	8.4	52.5	12	1	US-10-096-718-7	Sequence 7, Appli
99	8.4	52.5	12	1	US-10-096-718-27	Sequence 27, Appl
100	8.4	52.5	12	1	US-10-670-011-387	Sequence 387, App
101	8.4	52.5	12	1	US-10-257-017B-277600	Sequence 277600,
102	8.4	52.5	12	1	US-10-257-017B-314171	Sequence 314171,
103	8.4	52.5	12	1	US-10-257-017B-322459	Sequence 322459,
104	8.4	52.5	12	1	US-10-758-451-654	Sequence 654, App
105	8.4	52.5	12	1	US-10-758-451-771	Sequence 771, App
106	8.4	52.5	12	1	US-10-764-957-387	Sequence 387, App

RESULT 2
US-10-291-230-19/c
; Sequence 19, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.A
; CURRENT APPLICATION NUMBER: US/10/291,230
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-230-19

Query Match 77.5%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGCGGCATCG 15
||| ||||| |||
Db 14 GCGGGCGGCGTCG 1

RESULT 3
US-10-291-249-19/c
; Sequence 19, Application US/10291249
; Publication No. US20030119041A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.B
; CURRENT APPLICATION NUMBER: US/10/291,249
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-249-19

Query Match 77.5%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGCGGCATCG 15
||| ||||| |||
Db 14 GCGGGCGGCGTCG 1

RESULT 4
US-10-712-672-1460/c
; Sequence 1460, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1460
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1460

Query Match 71.2%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 21;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
||| ||||| |||
Db 16 GCGGGCGGCATCG 4

RESULT 5
US-10-712-672-1461/c
; Sequence 1461, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1461
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1461

Query Match 71.2%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 21;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
||| ||||| |||
Db 14 GCGGGCGGCATCG 2

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RESULT 6
US-09-093-972C-695
; Sequence 695, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 695:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 695:
US-09-093-972C-695

Query Match          67.5%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGCGGGCGGCATCG 15
      || |||||
Db      1 GGAGGGCGGCATGG 14

RESULT 7
US-10-758-451-695
; Sequence 695, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
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; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 695
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-695

Query Match          67.5%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGCGGGCGGCATCG 15
      || |||||
Db      1 GGAGGGCGGCATGG 14

RESULT 8
US-09-093-972C-673
; Sequence 673, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 673:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 673:
US-09-093-972C-673
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Query Match 67.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCATCG 15
||| ||||| ||| |
Db 2 GGAGGGCGGCATGG 15

RESULT 9
US-09-093-972C-694
; Sequence 694, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 694:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 694:
US-09-093-972C-694

Query Match 67.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCATCG 15
||| ||||| ||| |
Db 1 GGAGGGCGGCATGG 14

RESULT 10
US-10-758-451-673

; Sequence 673, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-673

Query Match 67.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCATCG 15
||| ||||| |||| |
Db 2 GGAGGGCGGCATGG 15

RESULT 11
US-10-758-451-694
; Sequence 694, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 694
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-694

Query Match 67.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCATCG 15
||| ||||| |||| |
Db 1 GGAGGGCGGCATGG 14

RESULT 12
US-09-093-972C-697
; Sequence 697, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive

```
;
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 697:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 697:
US-09-093-972C-697

Query Match          65.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGCGGGCGGCAT 13
Db      1 GGAGGGCGGCAT 12

RESULT 13
US-10-758-451-697
; Sequence 697, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 697
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-697

Query Match          65.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 23;
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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGCGGGCGGCAT 13
Db      1 GGAGGGCGGCAT 12

RESULT 14
US-09-093-972C-675
; Sequence 675, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 675:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 675:
US-09-093-972C-675

Query Match          65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGCGGGCGGCAT 13
Db      2 GGAGGGCGGCAT 13

RESULT 15
US-09-093-972C-696
; Sequence 696, Application US/09093972C
; Publication No. US20030087845A1
```



```
;
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 696:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 696:
US-09-093-972C-696

Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCAT 13
Db 1 GGAGGGCGGCAT 12

RESULT 16
US-10-758-451-675
; Sequence 675, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQUENCES: 996
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 696:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 696:
US-09-093-972C-696
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 675
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-675

Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCAT 13
Db 2 GGAGGGCGGCAT 13

RESULT 17
US-10-758-451-696
; Sequence 696, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 696
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-696

Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCAT 13
Db 1 GGAGGGCGGCAT 12

RESULT 18
US-09-093-972C-652
; Sequence 652, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 696:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 696:
US-09-093-972C-696
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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 652:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 652:
US-09-093-972C-652

Query Match          65.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGGCGGCAT 13
   |||||||||
Db 3 GGAGGGCGGCAT 14

RESULT 19
US-09-093-972C-674
; Sequence 674, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
```

```
;
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 674:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 674:
US-09-093-972C-674

Query Match          65.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGGCGGCAT 13
   |||||||||
Db 2 GGAGGGCGGCAT 13

RESULT 20
US-10-758-451-652
; Sequence 652, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 652
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-758-451-652

Query Match          65.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGGCGGCAT 13
   |||||||||
Db 3 GGAGGGCGGCAT 14

RESULT 21
US-10-758-451-674
; Sequence 674, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 674
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; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-674

Query Match      65.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGCGGGCGGCAT 13
      || |||||
Db      2 GGAGGGCGGCAT 13

RESULT 22
US-10-487-934-312/c
; Sequence 312, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-312

Query Match      62.5%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCGGGCGGCA 12
      |||||
Db      10 GCGGGCGGCA 1

RESULT 23
US-10-091-281-458
; Sequence 458, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 458
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative SPIF/SP1.01 motif
US-10-091-281-458

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-674

Query Match      65.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGCGGGCGGCAT 13
      || |||||
Db      2 GGAGGGCGGCAT 13

RESULT 22
US-10-487-934-312/c
; Sequence 312, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-312

Query Match      62.5%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCGGGCGGCA 12
      |||||
Db      10 GCGGGCGGCA 1

RESULT 23
US-10-091-281-458
; Sequence 458, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 458
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative SPIF/SP1.01 motif
US-10-091-281-458

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-674

Query Match      65.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGCGGGCGGC 11
      |||||
Db      1 GGCGGGCGGC 10

RESULT 24
US-10-257-017B-100005
; Sequence 100005, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 100005
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024859
US-10-257-017B-100005

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGCGGGCGGC 11
      |||||
Db      1 GGCGGGCGGC 10

RESULT 25
US-10-257-017B-100006/c
; Sequence 100006, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 100006
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024859
US-10-257-017B-100006

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGCGGGCGGC 11
      |||||
Db      13 GGCGGGCGGC 4

RESULT 26
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US-10-257-017B-229445
; Sequence 229445, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229445
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055973
US-10-257-017B-229445

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGCGGGCGG 10
Db      4 CGGCGGGCGG 13

RESULT 27
US-10-257-017B-229446/c
; Sequence 229446, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229446
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055973
US-10-257-017B-229446

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGCGGGCGG 10
Db      4 CGGCGGGCGG 13

RESULT 28
US-10-257-017B-229447
; Sequence 229447, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
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; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229447
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055973
US-10-257-017B-229447

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGCGGGCGG 10
Db      4 CGGCGGGCGG 13

RESULT 29
US-10-257-017B-229448/c
; Sequence 229448, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229448
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055973
US-10-257-017B-229448

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGCGGGCGG 10
Db      10 CGGCGGGCGG 1

RESULT 30
US-09-093-972C-716
; Sequence 716, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
```


; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 716:
US-09-093-972C-716

Query Match 61.2%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
| | | | | | | | |
Db 1 GAGGGCGGCATGG 13

RESULT 31
US-10-758-451-716
; Sequence 716, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 716
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-716

Query Match 61.2%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
| | | | | | | | |
Db 1 GAGGGCGGCATGG 13

RESULT 32
US-09-504-231A-1425/c
; Sequence 1425, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1425
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1425

Query Match 61.3%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCAT 13
| | | | | | | | |
Db 13 CGGCGAGCTGCAT 1

RESULT 33
US-09-274-553D-1425/c
; Sequence 1425, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1425
; LENGTH: 14
; TYPE: RNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1425

Query Match          61.3%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCAT 13
    ||||| || |||||
Db 13 CGGCGAGCTGCAT 1

RESULT 34
US-09-093-972C-715
; Sequence 715, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 715:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 715:

US-09-093-972C-715

Query Match          61.2%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
    | ||||| ||||| |
```

```

Db 1 GAGGGCGGCATGG 13

RESULT 35
US-10-758-451-715
; Sequence 715, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 715
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-715

Query Match          61.2%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
    | ||||| ||||| |
Db 1 GAGGGCGGCATGG 13

RESULT 36
US-09-093-972C-698
; Sequence 698, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 715:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 715:

US-09-093-972C-715

Query Match          61.2%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
    | ||||| ||||| |
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 698:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 698:
US-09-093-972C-698

Query Match      58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GCGGGCGGCA 12
      || |||||
Db      1 GGAGGCGGCA 11

RESULT 37
US-09-093-972C-718
; Sequence 718, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 718:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 718:
US-09-093-972C-718

Query Match      58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GCGGGCGGCA 12
      || |||||
Db      1 GGAGGCGGCA 11

US-09-093-972C-718
; Sequence 718, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 718:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 718:
US-09-093-972C-718

Query Match      58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCGGGCGCATCG 15
      |||||
Db      1 GCGGGCGCATCG 11
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;
; SEQUENCE DESCRIPTION: SEQ ID NO: 718:
US-09-093-972C-718

Query Match      58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 GCGGGCGGCAT 13
      |||||
Db      1 GAGGGCGGCAT 11

RESULT 38
US-09-093-972C-755
; Sequence 755, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 755:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 755:
US-09-093-972C-755

Query Match      58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCGGGCGCATCG 15
      |||||
Db      1 GCGGGCGCATCG 11
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Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGCGGCA 12
||| |||||
Db 2 GGAGGCGGCA 12

RESULT 43
US-09-093-972C-717
; Sequence 717, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 717:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 717:
US-09-093-972C-717

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGCGGCGCAT 13
| |||||
Db 1 GAGGCGGCGCAT 11

RESULT 44

US-09-093-972C-736
; Sequence 736, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 736:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 736:
US-09-093-972C-736

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGCGCGGCATCG 15
||| |||||
Db 2 GGCGCGGCATGG 12

RESULT 45
US-09-093-972C-754
; Sequence 754, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

;
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 754:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 754:
US-09-093-972C-754

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGGCATCG 15
||| ||| ||| |||
Db 1 GGGCGGCATGG 11

RESULT 46
US-10-758-451-676
; Sequence 676, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 676
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-676

Query Match 58.7%; Score 9.4; DB 1; Length 12;

Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGCGGCA 12
|| ||| ||| |||
Db 2 GGAGGGCGGCA 12

RESULT 47
US-10-758-451-717
; Sequence 717, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 717
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-717

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCAT 13
| ||| ||| |||
Db 1 GAGGGCGGCAT 11

RESULT 48
US-10-758-451-736
; Sequence 736, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 736
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-736

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGGCATCG 15
||| ||| ||| |||
Db 2 GGGCGGCATGG 12

RESULT 49
US-10-758-451-754
; Sequence 754, Application US/10758451

Publication No. US20050014711A1
GENERAL INFORMATION:
APPLICANT: East Carolina University
TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCOCONSTRICTION, ALLERGY (IES)
TITLE OF INVENTION: INFLAMMATION
FILE REFERENCE: 30775-706.301
CURRENT APPLICATION NUMBER: US/10/758,451
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 09/093,972
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 996
SOFTWARE: PatentIn version 3.1
SEQ ID NO 754
LENGTH: 12
TYPE: DNA
ORGANISM: Homo sapiens
US-10-758-451-754

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGCGGGCATCG 15
|||||||
Db 1 GGCGGGCATGG 11

RESULT 50
US-09-093-972C-653
Sequence 653, Application US/09093972C
Publication No. US20030087845A1
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 653:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 653:
US-09-093-972C-653

LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 653:
US-09-093-972C-653
Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGCGGGCGGCA 12
|||
Db 3 GGAGGGCGGCA 13

RESULT 51
US-09-093-972C-735
Sequence 735, Application US/09093972C
Publication No. US20030087845A1
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 735:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 735:
US-09-093-972C-735

Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCGGCATCG 15
| | | | | | | | | |
Db 2 GGGCGGCATGG 12

RESULT 52

US-09-093-972C-753
; Sequence 753, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:

; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998

; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 753:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 753:
US-09-093-972C-753

Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred.No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 5 GGGCGGCATCG 15
| | | | | | | | | |
Db 1 GGGCGGCATGG 11

RESULT 53

US-10-257-017B-227179
; Sequence 227179, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 227179
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006410
US-10-257-017B-227179

Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred.No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGGCGGCAT 13
| | | | | | | | | |
Db 2 GCGGGCGGTAT 12

RESULT 54

US-10-257-017B-227180/c
; Sequence 227180, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 227180
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0006410
US-10-257-017B-227180

Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred.No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGGCGGCAT 13
| | | | | | | | | |
Db 12 GCGGGCGGTAT 2

RESULT 55

US-10-758-451-653
; Sequence 653, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:

; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14

;
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 653
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-653

Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGCGGCGGCA 12
||| |||||
Db 3 GGAGGCGGCGCA 13

RESULT 56
US-10-758-451-735
; Sequence 735, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCOCONSTRUCTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 735
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-735

Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCGGCGCATCG 15
||| |||||
Db 2 GGGCGGCGCATGG 12

RESULT 57
US-10-758-451-753
; Sequence 753, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCOCONSTRUCTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 753
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-753

Query Match 58.7%; Score 9.4; DB 1; Length 13;

Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCGGCGCATCG 15
||| |||||
Db 1 GGGCGGCGCATGG 11

RESULT 58
US-09-093-972C-738
; Sequence 738, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRUCTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 738:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 738:
US-09-093-972C-738

Query Match 56.2%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGCGCAT 13
||| |||||
Db 2 GGGCGGCGCAT 10

RESULT 59
US-09-093-972C-756
; Sequence 756, Application US/09093972C

Publication No. US20030087845A1
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 756:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 756:
US-09-093-972C-756
Query Match 56.2%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCGGCAT 13
| | | | |
Db 1 GGGCGGCAT 9
RESULT 60
US-10-758-451-738
Sequence 738, Application US/10758451
Publication No. US20050014711A1
GENERAL INFORMATION:
APPLICANT: East Carolina University
TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCOCONSTRICTION, ALLERGY(IES)
TITLE OF INVENTION: INFLAMMATION
FILE REFERENCE: 30775-706.301
CURRENT APPLICATION NUMBER: US/10/758,451
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 09/093,972
PRIOR FILING DATE: 1998-06-09

NUMBER OF SEQ ID NOS: 996
SOFTWARE: PatentIn version 3.1
SEQ ID NO 738
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-758-451-738
Query Match 56.2%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCGGCAT 13
| | | | |
Db 2 GGGCGGCAT 10
RESULT 61
US-10-758-451-756
Sequence 756, Application US/10758451
Publication No. US20050014711A1
GENERAL INFORMATION:
APPLICANT: East Carolina University
TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCOCONSTRICTION, ALLERGY(IES)
TITLE OF INVENTION: INFLAMMATION
FILE REFERENCE: 30775-706.301
CURRENT APPLICATION NUMBER: US/10/758,451
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 09/093,972
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 996
SOFTWARE: PatentIn version 3.1
SEQ ID NO 756
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-758-451-756
Query Match 56.2%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCGGCAT 13
| | | | |
Db 1 GGGCGGCAT 9
RESULT 62
US-09-093-972C-737
Sequence 737, Application US/09093972C
Publication No. US20030087845A1
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998

;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 737:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 737:
US-09-093-972C-737

Query Match 56.2%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGCAT 13
| | | | |
Db 2 GGGCGGCAT 10

RESULT 63
US-10-758-451-737
; Sequence 737, Application US/10758451
; Publication No. US20050014711a1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 737
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-737

Query Match 56.2%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGCAT 13
| | | | |
Db 2 GGGCGGCAT 10

RESULT 64
US-09-739-068-13
; Sequence 13, Application US/09739068
; Patent No. US20020142297A1
; GENERAL INFORMATION:

;
; APPLICANT: Bogdanov, Alexei A.
; Weissleder, Ralph
; Simonova, Maria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMAGING
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,068
; FILING DATE: 18-Dec-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,366B
; FILING DATE: 29-JAN-1998
; APPLICATION NUMBER: 60/037,350
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 00786/388002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-739-068-13

Query Match 56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCGGCGG 10
| | | | |
Db 2 GCGCGGCGG 10

RESULT 65
US-10-091-281-459/c
; Sequence 459, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 459
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative AP2F/AP2.01 motif
US-10-091-281-459

Query Match 56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
| | | | | | | | | |
Db 9 CGGCGGGCG 1

RESULT 66
US-10-257-017B-269661/c
; Sequence 269661, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 269661
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001842
US-10-257-017B-269661

Query Match 56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGCGG 10
| | | | | | | | | |
Db 11 GCGGGGCGG 3

RESULT 67
US-10-257-017B-289845/c
; Sequence 289845, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 289845
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014116
US-10-257-017B-289845

Query Match 56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
| | | | | | | | | |

Db 11 CGGCGGGCG 3

RESULT 68
US-10-257-017B-322850
; Sequence 322850, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322850
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322850

Query Match 56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
| | | | | | | | | |
Db 3 CGGCGGGCG 11

RESULT 69
US-10-257-017B-322854
; Sequence 322854, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322854
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322854

Query Match 56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
| | | | | | | | | |
Db 3 CGGCGGGCG 11

RESULT 70
US-10-257-017B-322858
; Sequence 322858, Application US/10257017B
; Publication No. US20040241651A1


```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322858
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322858

Query Match          56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
Db 3 CGGCGGGCG 11

RESULT 71
US-10-257-017B-322859
; Sequence 322859, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322859
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322859

Query Match          56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
Db 3 CGGCGGGCG 11

RESULT 72
US-10-257-017B-299697/c
; Sequence 299697, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299697
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018689
US-10-257-017B-299697

Query Match          55.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGGCGGCATCGT 16
Db 12 GGGCGGGATGGT 1

RESULT 73
US-10-257-017B-311797
; Sequence 311797, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 311797
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0024693
US-10-257-017B-311797

Query Match          55.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCGGGCGCAT 13
Db 1 GGTGGGGCGCGT 12

RESULT 74
US-09-093-972C-699
; Sequence 699, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
```

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 699:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 699:
US-09-093-972C-699

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGC 11
|||
Db 1 GGAGGGCGGC 10

RESULT 75
US-09-093-972C-719
; Sequence 719, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: EPI-00672
; REFERENCE/DOCKET NUMBER: EPI-00672
; FILING DATE: 7-June-1995

;
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 719:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 719:
US-09-093-972C-719

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCA 12
|||
Db 1 GAGGGCGGCA 10

RESULT 76
US-09-093-972C-773
; Sequence 773, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 773:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 773:
US-09-093-972C-773

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 6 GCGGGCATCG 15
| | | | | | | | | |
Db 1 GCGGGCATGG 10

RESULT 77

US-10-113-877-39/c
; Sequence 39, Application US/10113877
; Publication No. US20020177218A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Yu
; APPLICANT: Wang, Xiao-Yang
; APPLICANT: Turpin, Pierre
; TITLE OF INVENTION: Methods of detecting multiple DNA
; TITLE OF INVENTION: binding protein and DNA interactions in a sample, and
; TITLE OF INVENTION: devices, systems and kits for practicing the same.
; FILE REFERENCE: CLON-071
; CURRENT APPLICATION NUMBER: US/10/113,877
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/280,658
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/314,330
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-113-877-39

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 CGCGGGCGG 10
| | | | | | | | | |
Db 10 CGCGGGCGG 1

RESULT 78

US-10-146-354A-4
; Sequence 4, Application US/10146354A
; Publication No. US20030054381A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Seymour, Albert B.
; APPLICANT: Nelson, Darcy L.
; APPLICANT: Webb, Suzin M.
; APPLICANT: Affourtit, Jason P.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND
; FILE REFERENCE: PC10461AGPR
; CURRENT APPLICATION NUMBER: US/10/146,354A

; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/293,425
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-354A-4

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 3 GCGGGCGGCA 12
| | | | | | | | | |
Db 1 GCGGACGGCA 10

RESULT 79

US-10-356-792-27/c
; Sequence 27, Application US/10356792
; Publication No. US20030215842A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej
; APPLICANT: Schweikhardt, Gary
; TITLE OF INVENTION: METHOD FOR THE ANALYSIS OF CYTOSINE METHYLATION PATTERNS
; FILE REFERENCE: 47675-33
; CURRENT APPLICATION NUMBER: US/10/356,792
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 60/352,944
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: AP-PCR Primer G6
US-10-356-792-27

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 4 CGGGCGGCAT 13
| | | | | | | | | |
Db 10 CGGGCGGCAT 1

RESULT 80

US-10-602-494-366/c
; Sequence 366, Application US/10602494
; Publication No. US20040265833A1
; GENERAL INFORMATION:
; APPLICANT: Cathy Lofton-Day
; APPLICANT: Andrew Sledziewski
; APPLICANT: Jeff Thomas
; APPLICANT: Robert W. Day
; APPLICANT: Lori Tonnes-Priddy
; APPLICANT: Karen Cardon
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of colorectal cell
; FILE REFERENCE: 47675-45
; CURRENT APPLICATION NUMBER: US/10/602,494
; CURRENT FILING DATE: 2003-06-23
; NUMBER OF SEQ ID NOS: 385
; SEQ ID NO 366
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo Sapiens

US-10-602-494-366

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGGGCGGCAT 13
| | | | | | | |
Db 10 CGGGCGGGAT 1

RESULT 81
US-10-758-451-699
; Sequence 699, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 699
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-699

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGGCGGC 11
| | | | | | | |
Db 1 GGAGGGCGGC 10

RESULT 82
US-10-758-451-719
; Sequence 719, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 719
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-719

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGGCGGCA 12
| | | | | | | |
Db 1 GAGGGCGGCA 10

RESULT 83
US-10-758-451-773
; Sequence 773, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 773
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-773

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCGGCATCG 15
| | | | | | | |
Db 1 GGCGGCATGG 10

RESULT 84
US-08-944-410-79/c
; Sequence 79, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-79

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGG 10
| | | | | | | |
Db 11 CGGAGGGCGG 2

RESULT 85
US-09-974-143A-10/c
; Sequence 10, Application US/09974143A
; Publication No. US20030022326A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; APPLICANT: Ose, Asuka
; TITLE OF INVENTION: NOVEL FETAL GENES
; FILE REFERENCE: 06501-089001
; CURRENT APPLICATION NUMBER: US/09/974,143A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: PCT/JP00/02281
; PRIOR FILING DATE: 2000-04-07

;; PRIOR APPLICATION NUMBER: JP 11/103356
;; PRIOR FILING DATE: 1999-04-09
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10
;; LENGTH: 11
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificially synthesized adapter sequence
US-09-974-143A-10

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGCGGGCGG 10
||| |||||
Db 11 CGGAGGCGG 2

RESULT 86

US-09-972C-677
; Sequence 677, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:

;; APPLICANT: Nyce, Jonathan W.
;; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
;; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
;; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

;; NUMBER OF SEQUENCES: 996

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

;; STREET: 7 Clarke Drive

;; CITY: Cranbury

;; STATE: New Jersey

;; COUNTRY: USA

;; ZIP: 08512

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/093,972C

;; FILING DATE: 09-Jun-1998

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/472,527

;; FILING DATE: 7-June-1995

;; APPLICATION NUMBER: US 08/757,024

;; FILING DATE: 26-11-1996

;; APPLICATION NUMBER: US 08/472,527

;; FILING DATE: 7-June-1995

;; APPLICATION NUMBER: US 09/016,464

;; FILING DATE: 30-January-1998

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Amzel, Viviana

;; REGISTRATION NUMBER: 30,930

;; REFERENCE/DOCKET NUMBER: EPI-00672

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 609-409-3035

;; TELEFAX: 413-254-9245

;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 677:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 11 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)

;; SEQUENCE DESCRIPTION: SEQ ID NO: 677:

US-09-972C-677

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGGCGGC 11
||| |||||
Db 2 GGAGGCGGC 11

RESULT 87

US-09-993-972C-772

; Sequence 772, Application US/09093972C

; Publication No. US20030087845A1

; GENERAL INFORMATION:

;; APPLICANT: Nyce, Jonathan W.

;; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
;; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
;; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

;; NUMBER OF SEQUENCES: 996

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

;; STREET: 7 Clarke Drive

;; CITY: Cranbury

;; STATE: New Jersey

;; COUNTRY: USA

;; ZIP: 08512

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/093,972C

;; FILING DATE: 09-Jun-1998

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/472,527

;; FILING DATE: 7-June-1995

;; APPLICATION NUMBER: US 08/757,024

;; FILING DATE: 26-11-1996

;; APPLICATION NUMBER: US 08/472,527

;; FILING DATE: 7-June-1995

;; APPLICATION NUMBER: US 09/016,464

;; FILING DATE: 30-January-1998

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Amzel, Viviana

;; REGISTRATION NUMBER: 30,930

;; REFERENCE/DOCKET NUMBER: EPI-00672

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 609-409-3035

;; TELEFAX: 413-254-9245

;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 772:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 11 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)

;; SEQUENCE DESCRIPTION: SEQ ID NO: 772:

US-09-993-972C-772

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCGGCATCG 15
||| |||||
Db 1 GGCGGCATGG 10

RESULT 88

US-10-112-267-44/c
; Sequence 44, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 44
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-11
; OTHER INFORMATION: Sequence is synthesized
US-10-112-267-44

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGG 10
||| |||||
Db 11 CGGAGGGCGG 2

RESULT 89
US-10-214-417A-45
; Sequence 45, Application US/10214417A
; Publication No. US20030162190A1
; GENERAL INFORMATION:
; APPLICANT: GORENSTEIN, DAVID G.
; APPLICANT: LUXON, BRUCE A.
; APPLICANT: HERZOG, NORBERT
; APPLICANT: YANG, XIAN BIN
; TITLE OF INVENTION: PHOSPHOROMONOTHIOATE AND PHOSPHORODITHIOATE
; FILE REFERENCE: UTMB:1011
; CURRENT APPLICATION NUMBER: US/10/214,417A
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/334,887
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-214-417A-45

US-10-434-588-41/c
; Sequence 41, Application US/10434588
; Publication No. US20030171557A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-Ichi
; APPLICANT: Oku, Asuka
; TITLE OF INVENTION: NOVEL SERINE-THREONINE KINASE GENE
; FILE REFERENCE: 06501-033002
; CURRENT APPLICATION NUMBER: US/10/434,588
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US/09/563,997
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/JP97/04855
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP 8-357864
; PRIOR FILING DATE: 1996-12-27
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-434-588-41

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGG 10
||| |||||
Db 11 CGGAGGGCGG 2

RESULT 91
US-10-628-770-24/c
; Sequence 24, Application US/10628770
; Publication No. US20040132052A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R1
; CURRENT APPLICATION NUMBER: US/10/628,770
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/182,562
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 24
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Artificial sequence
; LOCATION: 1-11
; OTHER INFORMATION: Sequence is synthesized
US-10-628-770-24

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGG 10
||| |||||
Db 11 CGGAGGGCGG 2

RESULT 92

US-10-762-154-32/c
; Sequence 32, Application US/10762154
; Publication No. US20040176574A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-Ichi
; APPLICANT: Oku, Asuka
; TITLE OF INVENTION: TRANSPORTER GENES
; FILE REFERENCE: 06501-057001
; CURRENT APPLICATION NUMBER: US/10/762,154
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US/09/521,195B
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: JP 10/156660
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 9/260972
; PRIOR FILING DATE: 1997-09-08
; PRIOR APPLICATION NUMBER: PCT/JP98/04009
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 32
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial Synthesized Adapter
US-10-762-154-32

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGG 10
||| |||||
Db 11 CGGAGGGCGG 2

RESULT 93

US-10-659-549-23/c
; Sequence 23, Application US/10659549
; Publication No. US20040229307A1
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/659,549
; FILING DATE: 10-Sep-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-659-549-23

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGG 10
||| |||||
Db 11 CGGAGGGCGG 2

RESULT 94

US-10-758-451-677
; Sequence 677, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 677
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-677

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGGGCGG 11
|| |||||
Db 2 GGAGGGCGG 11

RESULT 95

US-10-758-451-772
; Sequence 772, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 772
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-772

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GCGGGCATCG 15
||| ||||| |
Db 1 GCGGGCATGG 10

RESULT 96
US-09-093-972C-654
; Sequence 654, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 654:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 654:

US-09-093-972C-654

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGC 11
||| ||||| |
Db 3 GGAGGGCGGC 12

RESULT 97

US-09-093-972C-771
; Sequence 771, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 771:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 771:

US-09-093-972C-771

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GCGGGCATCG 15
||| ||||| |
Db 1 GCGGGCATGG 10

RESULT 98
US-10-096-718-7/c
; Sequence 7, Application US/10096718
; Publication No. US20030032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; CURRENT FILING DATE: 2002-03-12


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; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-096-718-7

Query Match          52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCGGCATCG 15
Db 10 GTCGGCATCG 1

RESULT 99
US-10-096-718-27
; Sequence 27, Application US/10096718
; Publication No. US20030032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-096-718-27

Query Match          52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCGGCATCG 15
Db 3 GTCGGCATCG 12

RESULT 100
US-10-670-011-387
; Sequence 387, Application US/10670011
; Publication No. US20040209832A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/132 (MBHB02-742-G)
; CURRENT APPLICATION NUMBER: US/10/670,011
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US60/386,782
; PRIOR FILING DATE: 2002-06-06
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; PRIOR APPLICATION NUMBER: US60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 427
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 387
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1
US-10-670-011-387

Query Match          52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGGCGGC 11
Db 1 GGCCGGCGGC 10

RESULT 101
US-10-257-017B-277600
; Sequence 277600, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 277600
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC00004520
US-10-257-017B-277600

Query Match          52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGGCGGC 11
Db 3 GGAGGGCGGC 12

RESULT 102
US-10-257-017B-314171
; Sequence 314171, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314171
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026157
US-10-257-017B-314171

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGG 10
||| |||||
Db 1 CGGAGGGCGG 10

RESULT 103

US-10-257-017B-322459/c
; Sequence 322459, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322459
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030884
US-10-257-017B-322459

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGG 10
||| ||||| ||
Db 11 CGGCGGGTGG 2

RESULT 104

US-10-758-451-654
; Sequence 654, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 654
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-654

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGGCGGC 11
|| |||||
Db 3 GGAGGGCGGC 12

RESULT 105

US-10-758-451-771
; Sequence 771, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 771
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-771

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCGGGCATCG 15
||| ||||| ||
Db 1 GCGGGCATGG 10

RESULT 106

US-10-764-957-387
; Sequence 387, Application US/10764957
; Publication No. US20050054596A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Pavco, Pamela
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/144 (MBHB02-742-O)
; CURRENT APPLICATION NUMBER: US/10/764,957
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US60/386,782

; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US60/408,378
; PRIOR FILING DATE: 2002-09-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 387
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF/VEGFR1 Homologous Target
US-10-764-957-387

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGC 11
| | | | |
Db 1 GGCGGGCGGC 10

RESULT 107

US-10-944-920-7/c
; Sequence 7, Application US/10944920
; Publication No. US20050136442A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/944,920
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US/10/096,718
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-944-920-7

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCGGCATCG 15
| | | | |
Db 10 GTCGGCATCG 1

RESULT 108

US-10-944-920-27
; Sequence 27, Application US/10944920
; Publication No. US20050136442A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/944,920

; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US/10/096,718
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-944-920-27

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCGGCATCG 15
| | | | |
Db 3 GTCGGCATCG 12

RESULT 109

US-10-869-055B-3
; Sequence 3, Application US/10869055B
; Publication No. US20050214782A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Tao
; APPLICANT: Li, Jinghan
; APPLICANT: Chen, Te-Ming
; TITLE OF INVENTION: Generation and application of standardized universal libraries
; FILE REFERENCE: 85201-232
; CURRENT APPLICATION NUMBER: US/10/869,055B
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: PCT/CA02/01941
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 60/340009
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: forward pcr primer
US-10-869-055B-3

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCGGCATCG 15
| | | | |
Db 3 GGCAGCATCG 12

RESULT 110

US-10-962-898-2263
; Sequence 2263, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/236 (MBHB02-742-U)
; CURRENT APPLICATION NUMBER: US/10/962,898
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/944,644
; PRIOR FILING DATE: 2004-09-16

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; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2263
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-962-898-2263

Query Match      52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGCGGGCGGC 11
      ||| |||||
Db      1 GGCGGGCGGC 10

RESULT 111
US-10-944-611-2263
; Sequence 2263, Application US/10944611
; Publication No. US20050233998A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/235 (MEHB02-742-S)
; CURRENT APPLICATION NUMBER: US/10/944,611
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
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; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2263
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-944-611-2263

Query Match      52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGCGGGCGGC 11
      ||| |||||
Db      1 GGCGGGCGGC 10

RESULT 112
US-09-154-750A-12/c
; Sequence 12, Application US/09154750A
; Publication No. US20020055097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGCGGGC 8
      |||||
Db      9 CGGCGGGC 2

RESULT 113
US-09-943-458-9/c
; Sequence 9, Application US/09943458
; Patent No. US20020110819A1
; GENERAL INFORMATION:
; APPLICANT: AVI BioPharma, Inc.
; TITLE OF INVENTION: Method for Analysis of Oligonucleotide
; TITLE OF INVENTION: Analogs
; FILE REFERENCE: 50450-8038.WO00
; CURRENT APPLICATION NUMBER: US/09/943,458
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,245
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
```


; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of complement to SEQ ID NO: 1
US-09-943-458-9

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCATCGT 16
| | | | | | | |
Db 10 GGCATCGT 3

RESULT 114
US-09-990-186-101
; Sequence 101, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-101

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCGG 10
| | | | | | | |
Db 1 GCGGGCGG 8

RESULT 115
US-09-990-186-1277
; Sequence 1277, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1277
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1277

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCGG 10
| | | | | | | |

Db 1 GCGGGCGG 8

RESULT 116
US-09-990-186-1688
; Sequence 1688, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1688
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1688

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGGGCGG 11
| | | | | | | |
Db 1 GCGGGCGG 8

RESULT 117
US-09-990-186-1689
; Sequence 1689, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1689
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1689

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGGGCGG 11
| | | | | | | |
Db 1 GCGGGCGG 8

RESULT 118
US-09-989-994-101
; Sequence 101, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

```
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-101

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCGGGCGG 10
        |||||
Db      1 GCGGGCGG 8

RESULT 119
US-09-989-994-1277
; Sequence 1277, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1277
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1277

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCGGGCGG 10
        |||||
Db      1 GCGGGCGG 8

RESULT 120
US-09-989-994-1688
; Sequence 1688, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1688
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
```

```
; OTHER INFORMATION: DNA
US-09-989-994-1688

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGGGCGGC 11
        |||||
Db      1 CGGGCGGC 8

RESULT 121
US-09-989-994-1689
; Sequence 1689, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1689
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1689

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGGGCGGC 11
        |||||
Db      1 CGGGCGGC 8

RESULT 122
US-10-033-145-1242
; Sequence 1242, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1242
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: DNA
US-10-033-145-1242

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGCGGGCG 9
        |||||
Db      3 GGCGGGCG 10
```

RESULT 123
US-10-033-145-1653
; Sequence 1653, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1653
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1653

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCATCGT 16
Db 1 GGCATCGT 8

RESULT 124
US-10-247-857-16/c
; Sequence 16, Application US/10247857
; Publication No. US20030115642A1
; GENERAL INFORMATION:
; APPLICANT: Rufty, Rebecca C.
; TITLE OF INVENTION: TOBACCO CULTIVAR NC 2000
; FILE REFERENCE: 5051-589
; CURRENT APPLICATION NUMBER: US/10/247,857
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,908
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Coupling marker
US-10-247-857-16

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGCA 12
Db 10 GGGCGGCA 3

RESULT 125
US-10-330-627-628
; Sequence 628, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319

; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-628

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGCG 9
Db 3 GGCGGGCG 10

RESULT 126
US-10-330-627-629
; Sequence 629, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 629
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-629

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGCG 9
Db 3 GGCGGGCG 10

RESULT 127
US-10-330-627-630
; Sequence 630, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-630

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGCGG 9
| | | | |
Db 3 GCGGGCGG 10

RESULT 128
US-10-228-876-1/c
; Sequence 1, Application US/10228876
; Publication No. US20040038400A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Allan C.
; APPLICANT: Loros, Jennifer J.
; APPLICANT: Dunlap, Jay C.
; TITLE OF INVENTION: METHODS FOR REGULATING GENE EXPRESSION USING LIGHT
; FILE REFERENCE: DC-0194
; CURRENT APPLICATION NUMBER: US/10/228,876
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-228-876-1

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGGCATC 14
| | | | |
Db 9 GCGGCATC 2

RESULT 129
US-10-301-875A-34/c
; Sequence 34, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-34

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
| | | | |
Db 10 CGGGCGGC 3

RESULT 130

US-10-713-381-21/c
; Sequence 21, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-21

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCGGC 8
| | | | |
Db 10 CGGGCGGC 3

RESULT 131
US-10-666-923-32
; Sequence 32, Application US/10666923
; Publication No. US20040235002A1
; GENERAL INFORMATION:
; APPLICANT: HOLMES, Michael
; APPLICANT: TSE, Christin
; TITLE OF INVENTION: MULTIPLEX SCREENING ASSAYS
; FILE REFERENCE: 8325-0033 (S33-US1)
; CURRENT APPLICATION NUMBER: US/10/666,923
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,345
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: ZFP 757 anxA8 binding site
US-10-666-923-32

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
| | | | |
Db 1 CGGGCGGC 8

RESULT 132
US-09-974-974-10/c
; Sequence 10, Application US/09974974
; Publication No. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA


```
;
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; TITLE OF INVENTION: target RNA by recognizing another molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: substrate
US-09-974-974-10

Query Match      48.8%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 79;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGGCGGGCGGC 11
      |||||
Db      11 CGGGGACGGC 1

RESULT 133
US-09-841-963A-5
; Sequence 5, Application US/09841963A
; Patent No. US20020081601A1
; GENERAL INFORMATION:
; APPLICANT: Watson, Dennis K.
; APPLICANT: Papas, Takis S. (Deceased)
; APPLICANT: Papas, Tula C. (Legal Representative)
; TITLE OF INVENTION: Methods and compositions for the diagnosis and treatment of cancer
; TITLE OF INVENTION: based on transcription factor ETS2
; FILE REFERENCE: 10545-015-999
; CURRENT APPLICATION NUMBER: US/09/841,963A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US99/27805
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 06/109,850
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-963A-5

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCGGCATCG 15
      |||||
Db      2 GCGGCATGG 10

RESULT 134
US-09-371-900-18/c
; Sequence 18, Application US/09371900
; Patent No. US20020137700A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
;
```

```
;
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/371,900
; FILING DATE: 11-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-371-900-18

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GCGGGCATC 14
      |||||
Db      10 GGCTGCATC 2

RESULT 135
US-09-970-820-18/c
; Sequence 18, Application US/09970820
; Patent No. US20020170077A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/970,820
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
;
```


RESULT 139
US-09-093-972C-678
; Sequence 678, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 678:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 678:
US-09-093-972C-678
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGCGGGCGG 10
Db 2 GGAGGGCGG 10
RESULT 140
US-09-093-972C-789
; Sequence 789, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996

CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 789:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 789:
US-09-093-972C-789
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GCGGCATCG 15
Db 1 GCGGCATCG 9
RESULT 141
US-09-989-994-1284
; Sequence 1284, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1284
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1284

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCGGCATCG 15
||| ||| |||
Db 1 GCGGCGTCG 9

RESULT 142

US-10-033-145-205/c
; Sequence 205, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 205
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-205

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
|| | ||| |||
Db 9 CGACGGGCG 1

RESULT 143

US-10-033-145-240
; Sequence 240, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-240

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
|| | ||| |||
Db 2 CGACGGGCG 10

RESULT 144

US-10-033-145-476/c
; Sequence 476, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 476
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-476

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGGCATCGT 16
||| | |||
Db 10 CGGCCTCGT 2

RESULT 145

US-10-329-465-129
; Sequence 129, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: FUSION
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-129

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
|| | ||| |||
Db 2 CGACGGGCG 10

RESULT 146

US-10-223-765-210
; Sequence 210, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun


```
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-210
```

```
Query Match          46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      5 GGGCGGCAT 13
        |||||
Db      2 GGGCGGGAT 10
```

RESULT 147

```
US-10-330-627-27/c
; Sequence 27, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-27
```

```
Query Match          46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      5 GGGCGGCAT 13
        |||||
Db      10 GGGCGGGAT 2
```

RESULT 148

```
US-10-330-627-57
; Sequence 57, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-57
```

```
Query Match          46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      4 CGGCGGGCA 12
        |||||
Db      1 CAGGCGGCA 9
```

RESULT 149

```
US-10-330-627-129/c
; Sequence 129, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-129
```

```
Query Match          46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      7 GCGGCATCG 15
        |||||
Db      9 GTGGCATCG 1
```

RESULT 150

```
US-10-330-627-239/c
; Sequence 239, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 239
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-239
```

```
Query Match          46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
QY      1 CGGCGGGCG 9
      || || || || ||
Db      9 CGACGGGCG 1

RESULT 151
US-10-330-627-407/c
; Sequence 407, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 407
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-407

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      6 GCGCGGCATC 14
      || || || || ||
Db      9 GGCAGCATC 1

RESULT 152
US-10-330-627-1318/c
; Sequence 1318, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1318
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1318

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      3 GCGGGCGGC 11
      || || || || ||
Db      10 GCCGGCGGC 2

RESULT 153
US-10-330-627-1346
; Sequence 1346, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1530
```

```
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1346
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1346

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 CGGCGGGCG 9
      || || || || ||
Db      2 CGACGGGCG 10

RESULT 154
US-10-330-627-1464/c
; Sequence 1464, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1464
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1464

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      3 GCGGGCGGC 11
      || || || || ||
Db      10 GCCGGCGGC 2

RESULT 155
US-10-330-627-1530/c
; Sequence 1530, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1530
```

```

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1530

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GCGGCGGC 11
Db      10 GCGGCGGC 2

RESULT 156
US-10-186-950-18/c
; Sequence 18, Application US/10186950
; Publication No. US20030188327A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/186,950
; FILING DATE: 02-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,496
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-186-950-18

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      6 GCGGCGCATC 14
Db      6 GCGGCGCATC 14
```

```

Db      10 GGCTGCATC 2

RESULT 157
US-10-314-578-1141/c
; Sequence 1141, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1141
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-1141

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CGGCATCGT 16
Db      9 CGACATCGT 1

RESULT 158
US-10-293-222-22/c
; Sequence 22, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-22

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GCGGCGCATC 14
Db      9 GGCAGCATC 1
```

```
RESULT 159
US-10-293-222-24/c
; Sequence 24, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-24
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGC 11
Db 10 GCCGGCGGC 2

RESULT 160
US-10-228-876-2/c
; Sequence 2, Application US/10228876
; Publication No. US20040038400A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Allan C.
; APPLICANT: Loros, Jennifer J.
; APPLICANT: Dunlap, Jay C.
; TITLE OF INVENTION: METHODS FOR REGULATING GENE EXPRESSION USING LIGHT
; FILE REFERENCE: DC-0194
; CURRENT APPLICATION NUMBER: US/10/228,876
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-228-876-2
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCGGCATCG 15
Db 9 GCGTCATCG 1

RESULT 161
US-10-301-875A-35/c
; Sequence 35, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-301-875A-35
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
Db 10 CGGCGGGCG 2

RESULT 162
US-10-301-875A-36/c
; Sequence 36, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-301-875A-36
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGGCGGGCA 12
Db 10 CGGCGGGCA 2

RESULT 163
US-10-758-451-678
; Sequence 678, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF I
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
```

```
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-301-875A-35
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
Db 10 CGGCGGGCG 2

RESULT 162
US-10-301-875A-36/c
; Sequence 36, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-301-875A-36
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGGCGGGCA 12
Db 10 CGGCGGGCA 2

RESULT 163
US-10-758-451-678
; Sequence 678, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF I
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
```



```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 678
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-678

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      2 GCGGGGCGG 10
      || |||||
Db      2 GGAGGGCGG 10

RESULT 164
US-10-758-451-789
; Sequence 789, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCOCONSTRUCTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 789
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-789

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      7 GCGGCATCG 15
      |||||
Db      1 GCGGCATGG 9

RESULT 165
US-10-805-292-164
; Sequence 164, Application US/10805292
; Publication No. US20050026176A1
; GENERAL INFORMATION:
; APPLICANT: Yoshii, Hiroto
; APPLICANT: Fukui, Toshifumi
; TITLE OF INVENTION: DNA PROBE DESIGNING APPARATUS AND INFORMATION PROCESSING METHOD
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 03560.003438
; CURRENT APPLICATION NUMBER: US/10/805,292
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: JPA2003-099464
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DNA exemplified in the drawing
US-10-805-292-164

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
```

```

Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 CGGCGGGCG 9
      |||||
Db      2 CGGCGGACG 10

RESULT 166
US-10-827-659-217/c
; Sequence 217, Application US/10827659
; Publication No. US20050235382A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: Docket number 38-21 (52710)C
; CURRENT APPLICATION NUMBER: US/10/827,659
; CURRENT FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-827-659-217

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      2 GCGGGGCGG 10
      || |||||
Db      10 GGGGGGCGG 2

RESULT 167
US-10-091-281-459
; Sequence 459, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 459
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative AP2F/AP2.01 motif
US-10-091-281-459

Query Match      45.0%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches      9; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

QY      1 CGGCGGGCGGCA 12
      || |||||
Db      1 CGCCCCCGCGCA 12

RESULT 168
US-09-758-073-5/c
; Sequence 5, Application US/09758073
; Patent No. US20010024785A1
; GENERAL INFORMATION:
; APPLICANT: Keinath, et al.
; TITLE OF INVENTION: Method of Diagnosing Gummy Stem Blight in
; TITLE OF INVENTION: Plants Using a Polymerase Chain Reaction Assay
```

```
;
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Judy C. Jarecki-Black, Ph.D.
; ADDRESSEE: Dority & Manning, P.A.
; STREET: 700 E. No. US20010024785A1th Street, Suite 15
; CITY: Greenville
; STATE: South Carolina
; COUNTRY: USA
; ZIP: 29601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS Dos; Windows 95
; SOFTWARE: WordPerfect 6.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,073
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/078,103
; FILING DATE: 16-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy C. Jarecki-Black, Ph.D.
; REGISTRATION NUMBER: P44,170
; REFERENCE/DOCKET NUMBER: CXU-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (864) 271-1592
; TELEFAX: (864) 233-7342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
; MOLECULE TYPE: Other Nucleic Acid
; DESCRIPTION: Oligonucleotide Primer
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE: Operon Technologies (Alameda, CA)
; IMMEDIATE SOURCE: Operon Technologies
; POSITION IN GENOME: No. US20010024785A1 Applicable
; UNITS:
; FEATURE:
; OTHER INFORMATION: Commercially Available Primer
; PUBLICATION INFORMATION: No. US20010024785A1 Applicable
;
; US-09-758-073-5
;
; Query Match 43.8%; Score 7; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1e+02;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 7 GCGGCAT 13
; Db 8 GCGGCAT 2
;
; RESULT 169
; US-09-811-259-4
; Sequence 4, Application US/09811259
; Patent No. US20020052483A1
; GENERAL INFORMATION:
; APPLICANT: Daniel K. Podolsky
; TITLE OF INVENTION: INTESTINAL TREFOIL PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```

```
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/811,259
; FILING DATE: 16-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/631,469
; FILING DATE: 12-APR-1996
; APPLICATION NUMBER: 08/191,352
; FILING DATE: 02-FEB-1994
; APPLICATION NUMBER: 08/037,741
; FILING DATE: 25-MAR-1993
; APPLICATION NUMBER: 07/837,192
; FILING DATE: 13-FEB-1992
; APPLICATION NUMBER: 07/655,965
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 00786/322001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200107
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
;
; US-09-811-259-4
;
; Query Match 43.8%; Score 7; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1e+02;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5 GGGCGGC 11
; Db 1 GGGCGGC 7
;
; RESULT 170
; US-09-789-996-45
; Sequence 45, Application US/09789996
; Publication No. US20030013119A1
; GENERAL INFORMATION:
; APPLICANT: Margolskee, Robert F.
; TITLE OF INVENTION: Gustducin Materials and Methods
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARSHALL, GERSTEIN & BORUN
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,996
; FILING DATE: 21-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/421,796
; FILING DATE: 10-OCT-1999
; APPLICATION NUMBER: US 08/124,807
; FILING DATE: 28-JUL-1998
; APPLICATION NUMBER: US 08/407,804
```

; FILING DATE: 20-MAR-1995
; APPLICATION NUMBER: US 08/045,801
; FILING DATE: 08-APR-1993
; APPLICATION NUMBER: US 07/868,353
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030013119Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 28038/37158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-789-996-45

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGCGGC 11
| | | | |
Db 1 GGCGGC 7

RESULT 171

US-09-990-186-1640
; Sequence 1640, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1640

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCGGCA 12
| | | | |
Db 3 GGCGGCA 9

RESULT 172

US-09-990-186-1641
; Sequence 1641, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1641
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1641

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGCGGCA 12
| | | | |
Db 3 GGCGGCA 9

RESULT 173

US-09-093-972C-843
; Sequence 843, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 843:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 843:
US-09-093-972C-843

```
Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGCGGGC 8
      |||||
Db      4 GGCGGGC 10

RESULT 174
US-09-093-972C-854
; Sequence 854, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 854:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 854:

US-09-093-972C-854

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGCGGGC 8
      |||||
Db      3 GGCGGGC 9

RESULT 175
US-09-093-972C-864
```

```
; Sequence 864, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 864:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 864:

US-09-093-972C-864

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGCGGGC 8
      |||||
Db      2 GGCGGGC 8

RESULT 176
US-09-093-972C-873
; Sequence 873, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
```


;
;
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 873:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 873:
US-09-093-972C-873

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
|||||
Db 1 GGCGGGC 7

RESULT 177
US-09-953-562-27
; Sequence 27, Application US/09953562
; Publication No. US20030096241A1
; GENERAL INFORMATION:
; APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.
; TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
; TITLE OF INVENTION: CELL CARCINOMA
; FILE REFERENCE: E6114-01
; CURRENT APPLICATION NUMBER: US/09/953,562
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: JP 2001-083352
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-953-562-27

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
|||||
Db 3 CGGCATC 9
;
RESULT 178
US-09-989-994-1640
; Sequence 1640, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1640

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
|||||
Db 3 GGCGGCA 9

RESULT 179
US-09-989-994-1641
; Sequence 1641, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1641
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1641

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
|||||
Db 3 GGCGGCA 9

RESULT 180
US-10-033-145-11/c
; Sequence 11, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION

```
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-11

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGCGGG 7
        |||||||
Db      8 CGGCGGG 2

RESULT 181
US-10-033-145-441/c
; Sequence 441, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 441
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-441

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCGGCAT 13
        |||||||
Db      8 GCGGCAT 2

RESULT 182
US-10-033-145-855/c
; Sequence 855, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 855
; SEQ ID NO 855
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-855

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GGGCGGC 11
        |||||||
Db      10 GGGCGGC 4

RESULT 183
US-10-033-145-1468
; Sequence 1468, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1468
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1468

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCGGGCG 9
        |||||||
Db      3 GCGGGCG 9

RESULT 184
US-10-033-145-1516/c
; Sequence 1516, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1516
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1516

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GCGGGCA 12
        |||||||
```

Db 8 GCGCGCA 2

RESULT 185
US-10-033-145-2124/c
; Sequence 2124, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2124
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2124

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGGG 7
|||||
Db 8 CCGCGGG 2

RESULT 186
US-10-141-263-5
; Sequence 5, Application US/10141263
; Publication No. US20020165196A1
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric
; TITLE OF INVENTION: Oligonucleotide Inhibitors of Cancer
; TITLE OF INVENTION: Cell Proliferation
; FILE REFERENCE: WIC01-NP003
; CURRENT APPLICATION NUMBER: US/10/141,263
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,166
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-141-263-5

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGGG 7
|||||
Db 2 CCGCGGG 8

RESULT 187
US-10-141-263-6/c
; Sequence 6, Application US/10141263
; Publication No. US20020165196A1
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric
; TITLE OF INVENTION: Oligonucleotide Inhibitors of Cancer

; TITLE OF INVENTION: Cell Proliferation
; FILE REFERENCE: WIC01-NP003
; CURRENT APPLICATION NUMBER: US/10/141,263
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,166
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-141-263-6

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGGG 7
|||||
Db 9 CCGCGGG 3

RESULT 188
US-10-313-642-5
; Sequence 5, Application US/10313642
; Publication No. US20030134797A1
; GENERAL INFORMATION:
; APPLICANT: Podolsky, Daniel K.
; TITLE OF INVENTION: Intestinal Trefoil Proteins
; FILE REFERENCE: 50206/432002
; CURRENT APPLICATION NUMBER: US/10/313,642
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/313,434
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for PCR
US-10-313-642-5

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCGGC 11
|||||
Db 1 GCGCGGC 7

RESULT 189
US-10-223-765-201
; Sequence 201, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22

```
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-201
```

```
Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 CGGCGGG 7
          |||||
Db       2 CGGCGGG 8
```

```
RESULT 190
US-10-330-627-367/c
; Sequence 367, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 367
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-367
```

```
Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 CGGCATC 14
          |||||
Db       10 CGGCATC 4
```

```
RESULT 191
US-10-330-627-384/c
; Sequence 384, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 384
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-384
```

```
Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGCGGGC 8
          |||||
Db       7 GGCGGGC 1
```

```
RESULT 192
US-10-330-627-923
; Sequence 923, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 923
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-923
```

```
Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 GGCGGGC 8
          |||||
Db       3 GGCGGGC 9
```

```
RESULT 193
US-10-330-627-924
; Sequence 924, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 924
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-924
```

```
Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 GGCGGGC 8
          |||||
Db       3 GGCGGGC 9
```

RESULT 194

US-10-330-627-938/c
; Sequence 938, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 938
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-938

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||
Db 9 GGGCGGC 3

RESULT 195
US-10-330-627-1120/c
; Sequence 1120, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1120
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1120

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||
Db 7 GGGCGGC 1

RESULT 196
US-10-356-792-21
; Sequence 21, Application US/10356792
; Publication No. US20030215842A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej
; APPLICANT: Schweikhardt, Gary
; TITLE OF INVENTION: METHOD FOR THE ANALYSIS OF CYTOSINE METHYLATION PATTERNS
; FILE REFERENCE: 47675-33
; CURRENT APPLICATION NUMBER: US/10/356,792
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 60/352,944

; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: AP-PCR Primer CG5
US-10-356-792-21

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||
Db 4 GGGCGGC 10

RESULT 197
US-10-259-723-2
; Sequence 2, Application US/10259723
; Publication No. US20030219764A1
; GENERAL INFORMATION:
; APPLICANT: Gene Networks, Inc.
; APPLICANT: Imoto, Seiya
; APPLICANT: Goto, Takao
; APPLICANT: Miyano, Satoru
; APPLICANT: Toshiro, Kosuke
; APPLICANT: Hoon, Michiel de
; APPLICANT: Savoie, Christopher J.
; APPLICANT: Kuhara, Satoru
; TITLE OF INVENTION: BIOLOGICAL DISCOVERY USING GENE REGULATORY NETWORKS GENERATED FROM
; TITLE OF INVENTION: MULTIPLE-DISRUPTION EXPRESSION LIBRARIES
; FILE REFERENCE: GENN1000US1
; CURRENT APPLICATION NUMBER: US/10/259,723
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/325,016
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/334,230
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/370,824
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/334,372
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/334,255
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/397,458
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-259-723-2

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
|||
Db 2 GGGCGGC 8

RESULT 198
US-10-353-334-4
; Sequence 4, Application US/10353334
; Publication No. US20030225250A1
; GENERAL INFORMATION:
; APPLICANT: Daniel K. Podolsky

;
;
; TITLE OF INVENTION: INTESTINAL TREFOIL PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/353,334
; FILING DATE: 29-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,469B
; FILING DATE: 12-Apr-1996
; APPLICATION NUMBER: 08/631,469
; FILING DATE: 12-APR-1996
; APPLICATION NUMBER: 08/191,352
; FILING DATE: 02-FEB-1994
; APPLICATION NUMBER: 08/037,741
; FILING DATE: 25-MAR-1993
; APPLICATION NUMBER: 07/837,192
; FILING DATE: 13-FEB-1992
; APPLICATION NUMBER: 07/655,965
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 00786/322001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200107
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-353-334-4

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
| | | | |
Db 1 GGGCGGC 7

RESULT 199
US-10-293-222-190/c
; Sequence 190, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29

;
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 190
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-190

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
| | | | |
Db 10 CGGCATC 4

RESULT 200
US-10-301-875A-9/c
; Sequence 9, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-9

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
| | | | |
Db 9 GGGCGGC 3

RESULT 201
US-10-301-875A-20/c
; Sequence 20, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-20

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
| | | | |
Db 10 GGGCGGC 4

RESULT 202

US-10-301-875A-33/c
; Sequence 33, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-33

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGG 7
| | | | |
Db 8 CGGCGGG 2

RESULT 203

US-10-794-929-32/c
; Sequence 32, Application US/10794929
; Publication No. US20040166526A1
; GENERAL INFORMATION:
; APPLICANT: OMNISCIENCE PHARMACEUTICALS
; APPLICANT: Chaparian, Michael
; APPLICANT: Zheng, Shu-Xian
; TITLE OF INVENTION: GENE CLONING
; FILE REFERENCE: 1002.00011
; CURRENT APPLICATION NUMBER: US/10/794,929
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 10/049,994
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/22743
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,788
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: 60/149,822
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: decamer OS-DEC-004

US-10-794-929-32

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
| | | | |
Db 10 GGGCGGC 4

RESULT 204

US-10-794-929-33/c
; Sequence 33, Application US/10794929
; Publication No. US20040166526A1
; GENERAL INFORMATION:
; APPLICANT: OMNISCIENCE PHARMACEUTICALS
; APPLICANT: Chaparian, Michael
; APPLICANT: Zheng, Shu-Xian
; TITLE OF INVENTION: GENE CLONING
; FILE REFERENCE: 1002.00011
; CURRENT APPLICATION NUMBER: US/10/794,929
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 10/049,994
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/22743
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,788
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: 60/149,822
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: decamer OS-DEC-005
US-10-794-929-33

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
| | | | |
Db 10 GGGCGGC 4

RESULT 205

US-10-602-494-360
; Sequence 360, Application US/10602494
; Publication No. US20040265833A1
; GENERAL INFORMATION:
; APPLICANT: Cathy Lofton-Day
; APPLICANT: Andrew Sledziewski
; APPLICANT: Jeff Thomas
; APPLICANT: Robert W. Day
; APPLICANT: Lori Tonnes-Priddy
; APPLICANT: Karen Cardon
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of colorectal cell
; FILE REFERENCE: 47675-45
; CURRENT APPLICATION NUMBER: US/10/602,494
; PRIOR FILING DATE: 2003-06-23
; NUMBER OF SEQ ID NOS: 385
; SEQ ID NO 360
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo Sapiens

US-10-602-494-360

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCGGGC 11
|||||||
Db 4 GGCGGGC 10

RESULT 206

US-10-758-451-843

; Sequence 843, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 843
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-758-451-843

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
|||||||
Db 4 GGCGGGC 10

RESULT 207

US-10-758-451-854

; Sequence 854, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 854
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-758-451-854

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
|||||||
Db 3 GGCGGGC 9

RESULT 208

US-10-758-451-864

; Sequence 864, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF I
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 864
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-758-451-864

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
|||||||
Db 2 GGCGGGC 8

RESULT 209

US-10-758-451-873

; Sequence 873, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF I
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 873
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-758-451-873

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
|||||||
Db 1 GGCGGGC 7

RESULT 210

US-10-497-764-27

; Sequence 27, Application US/10497764
; Publication No. US20050124598A1
; GENERAL INFORMATION:
; APPLICANT: Invenux, Inc.
; APPLICANT: Tarasow, Ted
; APPLICANT: Dewey, Torin
; APPLICANT: Eaton, Bruce
; APPLICANT: Nieuwlandt, Dan
; TITLE OF INVENTION: Antibiotic Compounds


```

; FILE REFERENCE: INX 2636-119PCT
; CURRENT APPLICATION NUMBER: US/10/497,764
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/340,255
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5' nucleotide is conjugated to diene reactant 13 or 14 via 2000MW
; OTHER INFORMATION: PEG linker
US-10-497-764-27

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGCGGG 7
      |||||
Db      4 CGGCGGG 10

RESULT 211
US-10-827-659-225/c
; Sequence 225, Application US/10827659
; Publication No. US20050235382A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: Docket number 38-21 (52710)C
; CURRENT APPLICATION NUMBER: US/10/827,659
; CURRENT FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-827-659-225

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GGGCGGC 11
      |||||
Db      10 GGGCGGC 4

Search completed: May 9, 2006, 16:47:25
Job time : 1 secs
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:49:14 ; Search time 0.001 Seconds
(without alignments)
6.912 Million cell updates/sec

Title: US-09-904-968A-20-COPY
Perfect score: 16
Sequence: 1 cggcggcgccgcgcgt 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 21 seqs, 216 residues

Total number of hits satisfying chosen parameters: 42

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 21 summaries

Database : pubnewdb20.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	8.4	52.5	11 1	US-10-512-214-4	Sequence 4, Appli
C 2	8.4	52.5	11 1	US-10-766-560-9	Sequence 9, Appli
C 3	8.4	52.5	11 1	US-11-182-592-10	Sequence 10, Appl
4	8	50.0	10 1	US-11-225-686-101	Sequence 101, App
5	8	50.0	10 1	US-11-225-686-1277	Sequence 1277, Ap
6	8	50.0	10 1	US-11-225-686-1688	Sequence 1688, Ap
7	8	50.0	10 1	US-11-225-686-1689	Sequence 1689, Ap
8	8	50.0	10 1	US-11-202-009-101	Sequence 101, App
9	8	50.0	10 1	US-11-202-009-1277	Sequence 1277, Ap
10	8	50.0	10 1	US-11-202-009-1688	Sequence 1688, Ap
11	8	50.0	10 1	US-11-202-009-1689	Sequence 1689, Ap
C 12	7.8	48.8	11 1	US-10-523-055-8	Sequence 8, Appli
C 13	7.8	48.8	11 1	US-11-158-209-104	Sequence 104, App
C 14	7.8	48.8	11 1	US-11-158-209-1201	Sequence 1201, Ap
15	7.4	46.3	10 1	US-11-225-686-1284	Sequence 1284, Ap
16	7.4	46.3	10 1	US-11-202-009-1284	Sequence 1284, Ap
17	7	43.8	10 1	US-10-962-756A-46	Sequence 46, Appl
18	7	43.8	10 1	US-11-225-686-1640	Sequence 1640, Ap
19	7	43.8	10 1	US-11-225-686-1641	Sequence 1641, Ap
20	7	43.8	10 1	US-11-202-009-1640	Sequence 1640, Ap
21	7	43.8	10 1	US-11-202-009-1641	Sequence 1641, Ap

ALIGNMENTS

RESULT 1
US-10-512-214-4/c
; Sequence 4, Application US/10512214
; Publication No. US20050255103A1
; GENERAL INFORMATION:
; APPLICANT: NEZU, Jun-ichi
; TITLE OF INVENTION: Therapeutic Reagent for Lung Carcinoma

; FILE REFERENCE: 382.1046
; CURRENT APPLICATION NUMBER: US/10/512,214
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: JP 2002-124743
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-512-214-4

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGCG 10
||| |||||
Db 11 CGGAGGGCGG 2

RESULT 2

US-10-766-560-9/c
; Sequence 9, Application US/10766560
; Publication No. US20050281837A1
; GENERAL INFORMATION:
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Bartoloni, Antonella
; TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE POLYPEPTIDES WITH ALTERED TOXICITY USEFUL
; TITLE OF INVENTION: PREPARATION OF AN ANTIPERTUSSIS VACCINE
; FILE REFERENCE: 002441.00076
; CURRENT APPLICATION NUMBER: US/10/766,560
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/261,668
; PRIOR FILING DATE: 1994-06-17
; PRIOR APPLICATION NUMBER: US 08/012,243
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/265,742
; PRIOR FILING DATE: 1988-11-01
; PRIOR APPLICATION NUMBER: ITALY 22481 A/87
; PRIOR FILING DATE: 1987-11-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Bordetella pertussis
US-10-766-560-9

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCGGCATCGT 16
||| |||||
Db 11 GCGGCTTCGT 2

RESULT 3

US-11-182-592-10/c
; Sequence 10, Application US/11182592
; Publication No. US20050250153A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; APPLICANT: Ose, Asuka
; TITLE OF INVENTION: NOVEL FETAL GENES
; FILE REFERENCE: 14875-089001 (previously 06501-089001)
; CURRENT APPLICATION NUMBER: US/11/182,592
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: US/09/974,143

```
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: PCT/JP00/02281
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 11/103356
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized adapter sequence
US-11-182-592-10

Query Match          52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGGGGCGG 10
      ||| |||||
Db      11 CGAGGGCGG 2

RESULT 4
US-11-225-686-101
; Sequence 101, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-101

Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCGGGCGG 10
      |||||
Db      1 GCGGGCGG 8

RESULT 5
US-11-225-686-1277
; Sequence 1277, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1277
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1277

Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCGGGCGG 10
      |||||
Db      1 GCGGGCGG 8

RESULT 6
US-11-225-686-1688
; Sequence 1688, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1688
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1688

Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGGGGGCG 11
      |||||
Db      1 CGGGGGCG 8

RESULT 7
US-11-225-686-1689
; Sequence 1689, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1689
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1689
```


Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
| | | | |
Db 1 CGGGCGGC 8

RESULT 8

US-11-202-009-101
; Sequence 101, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-11-202-009-101

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGGCGGC 10
| | | | |
Db 1 CGGGCGGC 8

RESULT 9

US-11-202-009-1277
; Sequence 1277, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1277
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-11-202-009-1277

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGGCGGC 10
| | | | |

Db 1 GCGGCGGC 8

RESULT 10

US-11-202-009-1688
; Sequence 1688, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1688
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-11-202-009-1688

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
| | | | |
Db 1 CGGGCGGC 8

RESULT 11

US-11-202-009-1689
; Sequence 1689, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1689
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-11-202-009-1689

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
| | | | |
Db 1 CGGGCGGC 8

RESULT 12

US-10-523-055-8/c
; Sequence 8, Application US/10523055
; Publication No. US20060057160A1

```
; GENERAL INFORMATION:
; APPLICANT: BIEMANS, Ralph
; APPLICANT: DENOEL, Philippe
; APPLICANT: FERON, Christiane
; APPLICANT: GORAJ, Carine
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: POOLMAN, Jan
; APPLICANT: WEYNANTS, Vincent
; TITLE OF INVENTION: VACCINE COMPOSITION COMPRISING
; TITLE OF INVENTION: LIPOOLIGOSACCHARIDE WITH REDUCED PHASE VARIABILITY
; FILE REFERENCE: B45309
; CURRENT APPLICATION NUMBER: US/10/523,055
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: PCT/EP03/008569
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: GB 0218037.0
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: GB 0218036.2
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: GB 0218035.4
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: GB 0218051.1
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: GB 0220197.8
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: GB 0220199.4
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: GB 0225524.8
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: GB 0225531.3
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: GB 0230164.6
; PRIOR FILING DATE: 2002-12-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-523-055-8
```

```
Query Match      48.8%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred.No. 5.6;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 GGGCGGCATCG 15
          |||||
Db      11 GGGCGGGGGCG 1
```

```
RESULT 13
US-11-158-209-104/c
; Sequence 104, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
```

```
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 104
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-104

Query Match      48.8%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred.No. 5.6;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGGGGGCGGCA 12
          |||||
Db      11 GGGGGGCAGCA 1

RESULT 14
US-11-158-209-1201/c
; Sequence 1201, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 1201
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-1201
```

```
Query Match      48.8%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred.No. 5.6;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGGGGGCGGCA 12
          |||||
Db      11 GCGGGGGGCCA 1
```

```
RESULT 15
US-11-225-686-1284
; Sequence 1284, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1284
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
```

```
; OTHER INFORMATION: DNA
US-11-225-686-1284

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GCGGCATCG 15
      ||||| |||
Db      1 GCGGCGTCG 9

RESULT 16
US-11-202-009-1284
; Sequence 1284, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1284
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-202-009-1284

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 GCGGCATCG 15
      ||||| |||
Db      1 GCGGCGTCG 9

RESULT 17
US-10-962-756A-46
; Sequence 46, Application US/10962756A
; Publication No. US2005025488A1
; GENERAL INFORMATION:
; APPLICANT: Aerssens, Jeroen
; APPLICANT: Athanasiou, Maria
; APPLICANT: Brain, Carlos
; APPLICANT: Cohen, Nadine
; APPLICANT: Dain, Bradley
; APPLICANT: Denton, R. Rex
; APPLICANT: Judson, Richard S.
; APPLICANT: Ozdemir, Vural
; APPLICANT: Reed, Carol R.
; TITLE OF INVENTION: NTRK1 Genetic Markers Associated with Age of Onset of Alzheimer's
; FILE REFERENCE: 2300.0020001
; CURRENT APPLICATION NUMBER: US/10/962,756A
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: US 60/511,247
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer Extension Oligonucleotides for Detecting Alleles a
```

```
; OTHER INFORMATION: t PSS in Haplotypes Comprising Preferred Embodiments of Age of C
; OTHER INFORMATION: set Markers I and I
US-10-962-756A-46

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CGGGCGG 10
      |||||
Db      2 CGGGCGG 8

RESULT 18
US-11-225-686-1640
; Sequence 1640, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1640

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GCGGGCA 12
      |||||
Db      3 GCGGGCA 9

RESULT 19
US-11-225-686-1641
; Sequence 1641, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1641
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1641

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Job time : 0.001 secs

QY 6 GGCGGCA 12
| | | | | | |
Db 3 GGCGGCA 9

RESULT 20
US-11-202-009-1640
; Sequence 1640, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-11-202-009-1640

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
| | | | | | |
Db 3 GGCGGCA 9

RESULT 21
US-11-202-009-1641
; Sequence 1641, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1641
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-11-202-009-1641

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
| | | | | | |
Db 3 GGCGGCA 9

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 53522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-968A-1

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Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
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Db      2043 CCATCCACCTGCTGTGTGACCTGGTAAAT 2071

RESULT 3
US-10-322-281-697
; Sequence 697, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697
; LENGTH: 34261
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(34261)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-697

Query Match      74.5%; Score 21.6; DB 7; Length 34261;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db      25406 CCCTCTACTTGCTGTGTGACCTGGAAAA 25433

RESULT 4
US-09-925-065A-336757
; Sequence 336757, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
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; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 336757
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-336757

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Best Local Similarity 82.8%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 5
US-09-925-065A-612157/c
; Sequence 612157, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 612157
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-612157

Query Match      72.4%; Score 21; DB 4; Length 339;
Best Local Similarity 82.8%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
      |||||
Db      77 CCACCCACTAGTTGTGTGACCTGGGAAAT 49

RESULT 6
US-10-027-632-25501
; Sequence 25501, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
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; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25501
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-25501

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Query Match 71.7%; Score 20.8; DB 5; Length 728;
Best Local Similarity 91.7%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGACCTGG 24
Db 173 CCCTCCACCTGCTGTGTGACCTTG 196

RESULT 7
US-10-027-632-25501
; Sequence 25501, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome

Query Match 71.7%; Score 20.8; DB 6; Length 728;
Best Local Similarity 91.7%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGACCTGG 24
Db 173 CCCTCCACCTGCTGTGACCTTG 196

RESULT 8
US-09-925-065A-589532/c
; Sequence 589532, Application US/09925065A

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; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589532
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589532-

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Query Match 71.0%; Score 20.6; DB 4; Length 551;
Best Local Similarity 85.2%; Pred. No. 39;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 403 ATTCACTTCTGTGTGACTTGGAAT 377

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RESULT 9
US-09-925-065A-589533/C
; Sequence 589533, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589533
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589533

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Query Match          71.0%; Score 20.6; DB 4; Length 551;
Best Local Similarity 85.2%; Pred. No. 39;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 3 ATCCACCTGTGTGTGACCTGGTAAAT 29
Db 403 ATTACACCTTCTGTGTGACCTTGGAAAT 377

Qy 4 TCCACCTGCTGTGTGACCTGGTAAA 28
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Db 87 TCCAACTACTGTGTGACCTGGGAAA 63

RESULT 14
US-09-925-065A-541706
; Sequence 541706, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541706
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-541706

Query Match 69.7%; Score 20.2; DB 4; Length 639;
Best Local Similarity 88.0%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTGTGACCTGGTAAA 28
| | | | | | | | | | | | | | | | | |
Db 607 TGCACCTGCTGTGTGACCTTCTAAA 631

RESULT 15
US-09-925-065A-541707
; Sequence 541707, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541707
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-541707

Query Match 69.7%; Score 20.2; DB 4; Length 639;
Best Local Similarity 88.0%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 TCCACCTGCTGTGTGACCTGGTAAA 28
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Db 607 TGCACCTGCTGTGTGACCTTCTAAA 631

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Scoring table: IDENTITY NUC
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19: /SID55/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21.6	74.5	1094	10	US-10-750-185-40770	Sequence 40770, A
2	21.6	74.5	1094	10	US-10-750-623-40770	Sequence 40770, A
3	21	72.4	336	7	US-09-925-065A-336757	Sequence 336757,
c 4	21	72.4	339	7	US-09-925-065A-612157	Sequence 612157,
5	21	72.4	345	12	US-10-301-480-410051	Sequence 410051,
6	21	72.4	345	12	US-10-301-480-1023460	Sequence 1023460,
c 7	20.6	71.0	551	7	US-09-925-065A-589532	Sequence 589532,
c 8	20.6	71.0	551	7	US-09-925-065A-589533	Sequence 589533,
c 9	20.4	70.3	598	7	US-09-925-065A-256045	Sequence 256045,
c 10	20.4	70.3	598	7	US-09-925-065A-256046	Sequence 256046,
c 11	20.4	70.3	609	12	US-10-301-480-334798	Sequence 334798,
c 12	20.4	70.3	609	12	US-10-301-480-334799	Sequence 334799,
c 13	20.4	70.3	609	12	US-10-301-480-948207	Sequence 948207,
c 14	20.4	70.3	609	12	US-10-301-480-948208	Sequence 948208,

c 15	20.2	69.7	610	7	US-09-925-065A-935980	Sequence 935980,
c 16	20.2	69.7	610	7	US-09-925-065A-935981	Sequence 935981,
17	20.2	69.7	639	7	US-09-925-065A-541706	Sequence 541706,
18	20.2	69.7	639	7	US-09-925-065A-541707	Sequence 541707,
19	20.2	69.7	13667	17	US-11-128-061-1065	Sequence 1065, Ap
20	20.2	69.7	13667	17	US-11-128-049-1065	Sequence 1065, Ap
21	20	69.0	201	10	US-10-995-561-65184	Sequence 65184, A
22	20	69.0	528	12	US-10-301-480-372169	Sequence 372169,
23	20	69.0	528	12	US-10-301-480-985578	Sequence 985578,
c 24	20	69.0	530	7	US-09-925-065A-295310	Sequence 295310,
c 25	20	69.0	557	7	US-09-925-065A-295309	Sequence 295309,
26	20	69.0	557	12	US-10-301-480-372168	Sequence 372168,
27	20	69.0	557	12	US-10-301-480-985577	Sequence 985577,
c 28	20	69.0	601	7	US-09-925-065A-884195	Sequence 884195,
c 29	20	69.0	601	7	US-09-925-065A-910370	Sequence 910370,
c 30	20	69.0	601	7	US-09-925-065A-910371	Sequence 910371,
c 31	20	69.0	605	7	US-09-925-065A-327159	Sequence 327159,
c 32	20	69.0	606	12	US-10-301-480-401205	Sequence 401205,
c 33	20	69.0	606	12	US-10-301-480-1014614	Sequence 1014614,
34	20	69.0	659	7	US-09-925-065A-785405	Sequence 785405,
35	20	69.0	659	7	US-09-925-065A-785406	Sequence 785406,
c 36	20	69.0	1050	10	US-10-750-185-50274	Sequence 50274, A
c 37	20	69.0	1050	10	US-10-750-623-50274	Sequence 50274, A
38	20	69.0	66916	10	US-10-995-561-13374	Sequence 13374, A
39	19.8	68.3	25667	11	US-10-330-773-422	Sequence 422, App
40	19.8	68.3	139573	12	US-10-506-513-3	Sequence 3, Appli
41	19.6	67.6	201	17	US-11-124-367A-24332	Sequence 24332, A
42	19.6	67.6	443	7	US-09-925-065A-463434	Sequence 463434,
43	19.6	67.6	590	7	US-09-925-065A-223323	Sequence 223323,
44	19.6	67.6	599	12	US-10-301-480-308284	Sequence 308284,
45	19.6	67.6	599	12	US-10-301-480-921693	Sequence 921693,

ALIGNMENTS

RESULT 1
US-10-750-185-40770
; Sequence 40770, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 40770
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Bovine 19866881093594
US-10-750-185-40770

Query Match 74.5%; Score 21.6; DB 10; Length 1094;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGACCTGGTAAA 28
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Db 1053 CCATTACCAGCTGTGTGACCTGAGAAA 1080

RESULT 2
US-10-750-623-40770

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; Sequence 40770, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 40770
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Bovine 19866881093594
US-10-750-623-40770

Query Match      74.5%; Score 21.6; DB 10; Length 1094;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CCATCCACCTGCTGTGTGACCTGGTAA 28
      |||| |||| |||| |||| |||| |||| ||||
Db     1053 CCATTCACGAGCTGTGTGACCTGAGAAA 1080

RESULT 3
US-09-925-065A-336757
; Sequence 336757, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 336757
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-336757

Query Match      72.4%; Score 21; DB 7; Length 336;
Best Local Similarity 82.8%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
      ||| ||| | |||| |||| |||| ||||
Db     263 CCACCCACTAGTTGTGTGACCTGGGAAAT 291

RESULT 4
US-09-925-065A-612157/c
```

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; Sequence 612157, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 612157
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-612157

Query Match      72.4%; Score 21; DB 7; Length 339;
Best Local Similarity 82.8%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
      ||| ||| | |||| |||| |||| ||||
Db     77 CCACCCACTAGTTGTGTGACCTGGGAAAT 49

RESULT 5
US-10-301-480-410051
; Sequence 410051, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 410051
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-410051

Query Match      72.4%; Score 21; DB 12; Length 345;
Best Local Similarity 82.8%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
      ||| ||| | |||| |||| |||| ||||
Db     263 CCACCCACTAGTTGTGTGACCTGGGAAAT 291

RESULT 6
US-10-301-480-1023460
; Sequence 1023460, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1023460
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1023460

Query Match 72.4%; Score 21; DB 12; Length 345;
Best Local Similarity 82.8%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
||| ||| | ||||| ||||| |||||
Db 263 CCACCCACTAGTGTGTGACCTGGGAAAT 291

RESULT 7
US-09-925-065A-589532/c
; Sequence 589532, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 589532
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589532

Query Match 71.0%; Score 20.6; DB 7; Length 551;
Best Local Similarity 85.2%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTGACCTGGTAAAT 29
||| ||| | ||||| ||||| |||||
Db 403 ATTCACCTTCTGTGTGACCTTGGAAAT 377

RESULT 8
US-09-925-065A-589533/c
; Sequence 589533, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 589533
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589533

Query Match 71.0%; Score 20.6; DB 7; Length 551;
Best Local Similarity 85.2%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTGACCTGGTAAAT 29
||| ||| | ||||| ||||| |||||
Db 403 ATTCACCTTCTGTGTGACCTTGGAAAT 377

RESULT 9
US-09-925-065A-256045/c
; Sequence 256045, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 256045
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-256045

Query Match 70.3%; Score 20.4; DB 7; Length 598;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||| | ||||| ||||| |||||
Db 561 CCTCCTGCTGTGTGACCTGGTA 540

RESULT 10
US-09-925-065A-256046/c
; Sequence 256046, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 256046
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-256046

Query Match 70.3%; Score 20.4; DB 7; Length 598;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 561 CCTCCTGCTGTGTGACCTGGTA 540

RESULT 11
US-10-301-480-334798/c
; Sequence 334798, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 334798
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-334798

Query Match 70.3%; Score 20.4; DB 12; Length 609;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 560 CCTCCTGCTGTGTGACCTGGTA 539

RESULT 12
US-10-301-480-334799/c
; Sequence 334799, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome

; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 334799
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-334799

Query Match 70.3%; Score 20.4; DB 12; Length 609;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 560 CCTCCTGCTGTGTGACCTGGTA 539

RESULT 13
US-10-301-480-948207/c
; Sequence 948207, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 948207
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-948207

Query Match 70.3%; Score 20.4; DB 12; Length 609;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 560 CCTCCTGCTGTGTGACCTGGTA 539

RESULT 14
US-10-301-480-948208/c
; Sequence 948208, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 948208
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-948208

Query Match 70.3%; Score 20.4; DB 12; Length 609;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 560 CCTCCTGCTGTGTGACCTGGTA 539

RESULT 15
US-09-925-065A-935980/c
; Sequence 935980, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 935980
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935980

Query Match 69.7%; Score 20.2; DB 7; Length 610;
Best Local Similarity 88.0%; Pred. No. 49;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTGACCTGGTAAA 28
||| ||| ||||| ||||| ||||| |||||
Db 87 TCCAACTACTGTGTGACCTGGGAAA 63

Search completed: May 9, 2006, 06:39:10
Job time : 656.044 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:14:10 ; Search time 71.6444 Seconds
(without alignments)
645.083 Million cell updates/sec

Title: US-09-904-968A-4
Perfect score: 26
Sequence: 1 ccacctatcgcccttcctaagcat 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	31571	2 US-08-323-443B-1	Sequence 1, Appli
C 2	26	100.0	53526	3 US-08-658-136-2	Sequence 2, Appli
C 3	26	100.0	53577	3 US-08-658-136-1	Sequence 1, Appli
C 4	26	100.0	53577	3 US-08-460-215A-1	Sequence 1, Appli
5	19.6	75.4	4403765	3 US-09-103-840A-2	Sequence 2, Appli
6	19.6	75.4	4411529	3 US-09-103-840A-1	Sequence 1, Appli
7	18.2	70.0	601	3 US-09-949-016-27337	Sequence 27337, A
8	18.2	70.0	601	3 US-09-949-016-63547	Sequence 63547, A
9	18.2	70.0	24709	3 US-09-949-016-12225	Sequence 12225, A
10	18.2	70.0	24710	3 US-09-949-016-12225	Sequence 13595, A
11	18.2	70.0	213456	3 US-09-949-016-13595	Sequence 3, Appli
12	18.2	70.0	323820	3 US-09-820-007-3	Sequence 14139, A
C 13	18	69.2	143	3 US-09-949-016-14139	Sequence 25080, A
14	18	69.2	27727	3 US-09-949-016-15737	Sequence 15737, A
C 15	18	69.2	32177	3 US-09-949-002-712	Sequence 712, App
16	17.8	68.5	601	3 US-09-949-016-82906	Sequence 82906, A
17	17.8	68.5	32998	3 US-09-408-020-1	Sequence 1, Appli
18	17.6	67.7	8000	3 US-09-415-784-101	Sequence 101, App
19	17.6	67.7	8000	3 US-09-415-784-102	Sequence 102, App
20	17.6	67.7	8000	3 US-09-415-785A-101	Sequence 101, App
21	17.6	67.7	8000	3 US-09-415-785A-102	Sequence 102, App
22	17.6	67.7	8000	3 US-08-944-465-101	Sequence 101, App
23	17.6	67.7	8000	3 US-08-944-465-102	Sequence 102, App
24	17.6	67.7	8000	3 US-09-415-868-101	Sequence 101, App

25	17.6	67.7	8000	3 US-09-415-868-102	Sequence 102, App
26	17.6	67.7	8000	3 US-09-415-900-101	Sequence 101, App
27	17.6	67.7	8000	3 US-09-415-900-102	Sequence 102, App
28	17.6	67.7	8000	3 US-09-507-362-101	Sequence 101, App
29	17.6	67.7	8000	3 US-09-507-362-102	Sequence 102, App
30	17.6	67.7	9951	3 US-09-193-707-3	Sequence 3, Appli
31	17.6	67.7	10524	3 US-09-193-707-4	Sequence 4, Appli
32	17.6	67.7	11282	3 US-09-733-042-1	Sequence 1, Appli
33	17.6	67.7	11703	2 US-08-801-263A-8	Sequence 8, Appli
34	17.6	67.7	11703	3 US-09-102-248-8	Sequence 8, Appli
35	17.6	67.7	11703	3 US-09-367-764-8	Sequence 8, Appli
36	17.6	67.7	11740	3 US-09-415-784-103	Sequence 103, App
37	17.6	67.7	11740	3 US-08-944-465-103	Sequence 103, App
38	17.6	67.7	11740	3 US-09-415-868-103	Sequence 103, App
39	17.6	67.7	11740	3 US-09-415-900-103	Sequence 103, App
40	17.6	67.7	11740	3 US-09-507-362-103	Sequence 103, App
41	17.6	67.7	11927	3 US-09-193-707-5	Sequence 5, Appli
42	17.6	67.7	13905	3 US-08-972-218-1	Sequence 1, Appli
43	17.6	67.7	13905	3 US-09-193-707-1	Sequence 1, Appli
44	17.6	67.7	13905	3 US-08-741-881-1	Sequence 1, Appli
45	17.6	67.7	16656	2 US-08-741-881-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-323-443B-1
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/OA462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

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; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match      100.0%; Score 26; DB 2; Length 31571;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACCTCATCGCCCTTCCTAAGCAT 26
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Db      2619 CCACCTCATCGCCCTTCCTAAGCAT 2644

RESULT 2
US-08-658-136-2/c
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match      100.0%; Score 26; DB 3; Length 53526;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACCTCATCGCCCTTCCTAAGCAT 26
      |||||||
Db      4315 CCACCTCATCGCCCTTCCTAAGCAT 4290

RESULT 3
US-08-658-136-1/c
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match      100.0%; Score 26; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACCTCATCGCCCTTCCTAAGCAT 26
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Db      4314 CCACCTCATCGCCCTTCCTAAGCAT 4289

RESULT 4
US-08-460-215A-1/c
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,215A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUGAN, DEBORAH
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-17.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-460-215A-1

Query Match 100.0%; Score 26; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26
|||||
Db 4314 CCACCTCATCGCCCTTCCTAAGCAT 4289

RESULT 5

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 75.4%; Score 19.6; DB 3; Length 4403765;
Best Local Similarity 84.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26
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Db 3008548 CCACCTCATCGGCCCTCCTTTGCAT 3008573

RESULT 6

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 75.4%; Score 19.6; DB 3; Length 4411529;
Best Local Similarity 84.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26
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Db 3013643 CCACCTCATCGGCCCTCCTTTGCAT 3013668

RESULT 7

US-09-949-016-27337
; Sequence 27337, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27337
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-27337

Query Match 70.0%; Score 18.2; DB 3; Length 601;
Best Local Similarity 87.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCTTCCTAAGCA 25
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Db 362 ACCTCTTAGCCCTTCCTCAGCA 384

RESULT 8

US-09-949-016-63547
; Sequence 63547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63547
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-63547

Query Match 70.0%; Score 18.2; DB 3; Length 601;
Best Local Similarity 87.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ACCTCATCGCCCTTCCTAAGCA 25
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Db 362 ACCTCTTAGCCCTTCCTCAGCA 384

RESULT 9
US-09-949-016-12225
; Sequence 12225, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12225
; LENGTH: 24709
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12225

Query Match 70.0%; Score 18.2; DB 3; Length 24709;
Best Local Similarity 87.0%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ACCTCATCGCCCTTCCTAAGCA 25
|||||
Db 19303 ACCTCTTAGCCCTTCCTCAGCA 19325

RESULT 10
US-09-949-016-13595
; Sequence 13595, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13595
; LENGTH: 24710
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13595

Query Match 70.0%; Score 18.2; DB 3; Length 24710;
Best Local Similarity 87.0%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ACCTCATCGCCCTTCCTAAGCA 25
|||||
Db 19303 ACCTCTTAGCCCTTCCTCAGCA 19325

RESULT 11
US-09-820-007-3
; Sequence 3, Application US/09820007
; Patent No. 6830900
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001205
; CURRENT APPLICATION NUMBER: US/09/820,007
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 213456
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(213456)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-007-3

Query Match 70.0%; Score 18.2; DB 3; Length 213456;
Best Local Similarity 87.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCTCATCGCCCTTCCTAAGCAT 26
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Db 184770 CCTCATCACTCTTCCAAAGCAT 184792

RESULT 12
US-09-949-016-14139
; Sequence 14139, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14139
; LENGTH: 323820
; TYPE: DNA
; ORGANISM: Human
; FEATURE:

Query Match 69.2%; Score 18; DB 3; Length 27727;
Best Local Similarity 80.8%; Pred. No. 1.1e+02;

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:26:49 ; Search time 629.489 Seconds
(without alignments)
341.553 Million cell updates/sec

Title: US-09-904-968A-4
Perfect score: 26
Sequence: 1 ccacctcatcgcccttcctaagcat 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	26	100.0	53522	3	US-09-904-968A-1
C 3	24.4	93.8	6423	6	US-10-240-485-121
C 4	19.6	75.4	80264	9	US-10-737-318-83
5	18.8	72.3	796	7	US-10-424-599-7186
C 6	18.2	70.0	537	4	US-09-925-065A-49324
C 7	18.2	70.0	537	4	US-09-925-065A-49325
8	18.2	70.0	569	4	US-09-925-065A-262314
9	18.2	70.0	569	4	US-09-925-065A-437738
10	18.2	70.0	569	4	US-09-925-065A-437739
11	18.2	70.0	569	4	US-09-925-065A-437740
12	18.2	70.0	5549	3	US-09-764-877-2860
13	18.2	70.0	5549	6	US-10-242-515-2860
14	18.2	70.0	58952	5	US-10-087-192-1690
15	18.2	70.0	213456	3	US-09-820-007-3
16	18.2	70.0	213456	9	US-10-981-724-3
17	18	69.2	352	8	US-10-357-930-59953
18	18	69.2	554	8	US-10-357-930-60566
C 19	18	69.2	575	4	US-09-925-065A-471791
C 20	18	69.2	631	7	US-10-437-963-97251
21	18	69.2	846	5	US-10-027-632-152758
22	18	69.2	846	6	US-10-027-632-152758
C 23	18	69.2	40000	8	US-10-741-600-18014

C 24	18	69.2	44990	7	US-10-052-482-217	Sequence 217, App
C 25	17.8	68.5	537	4	US-09-925-065A-49323	Sequence 49323, A
26	17.8	68.5	567	4	US-09-925-065A-590403	Sequence 590403,
27	17.8	68.5	569	4	US-09-925-065A-437741	Sequence 437741,
28	17.8	68.5	32998	5	US-10-027-806-1	Sequence 1, Appli
29	17.8	68.5	32998	5	US-10-034-623-1	Sequence 1, Appli
30	17.8	68.5	32998	5	US-10-027-801-1	Sequence 1, Appli
31	17.8	68.5	32998	6	US-10-029-120-1	Sequence 1, Appli
C 32	17.6	67.7	199	3	US-09-294-093B-4296	Sequence 4296, Ap
C 33	17.6	67.7	200	3	US-09-922-293-1399	Sequence 1399, Ap
34	17.6	67.7	256	6	US-10-029-386-14670	Sequence 14670, A
35	17.6	67.7	267	8	US-10-425-115-175164	Sequence 175164,
C 36	17.6	67.7	287	3	US-09-922-293-1398	Sequence 1398, Ap
38	17.6	67.7	533	6	US-10-029-386-967	Sequence 967, App
39	17.6	67.7	675	4	US-09-925-065A-502013	Sequence 502013,
C 40	17.6	67.7	754	8	US-10-425-115-84140	Sequence 84140, A
C 41	17.6	67.7	1089	9	US-10-343-477A-47	Sequence 47, Appl
C 42	17.6	67.7	1759	8	US-10-739-930-4071	Sequence 4071, Ap
43	17.6	67.7	1865	8	US-10-739-930-5444	Sequence 5444, Ap
44	17.6	67.7	8000	3	US-09-507-362-101	Sequence 101, App
45	17.6	67.7	8000	3	US-09-507-362-102	Sequence 102, App
			8000	6	US-10-391-441-101	Sequence 101, App

ALIGNMENTS

RESULT 1
US-09-904-968A-4
; Sequence 4, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer BPR9
US-09-904-968A-4

Query Match 100.0%; Score 26; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCCTCAAGCAT 26
|||||
Db 1 CCACCTCATCGCCCTTCCTCAAGCAT 26

RESULT 2
US-09-904-968A-1/c
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE

```

; FILE REFERENCE: JHUL680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A-1
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 53522
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-904-968A-1

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Query Match      100.0%; Score 26; DB 3; Length 53522;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CCACCTCATCGCCCTTCTTAAGCAT 26
4315 CCACCTCATCGCCCTTCTTAAGCAT 4290

RESULT 3
US-10-240-485-121/c
; Sequence 121, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 121
; LENGTH: 6423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo
US-10-240-485-121

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Query Match      93.8%; Score 24.4; DB 6; Length 6423;
Best Local Similarity 96.2%; Pred. No. 0.28;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CCACCTCATCGCCCTTCTCTAAGCAT 26
|||
Db 5876 CCACCTCATCGCCCTTCTCTAAGCAT 5851

RESULT 4
US-10-737-318-83/c
; Sequence 83, Application US/10737318
; Publication No. US20050202442A1
; GENERAL INFORMATION:
; APPLICANT: MORRIS, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER

```

; FILE REFERENCE: 529452002800
; CURRENT APPLICATION NUMBER: US/10/737,318
; CURRENT FILING DATE: 2003-12-15
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 80264
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(80264)
; OTHER INFORMATION: n = A,T,C or G
US-10-737-318-83

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Query Match      75.4%; Score 19.6; DB 9; Length 80264;
Best Local Similarity 84.6%; Pred. No. 43;
Matches 22: Conservative 0; Mismatches 4; Indels 0;
Gaps 0;

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Oy 1 CCACCTCATCGCCCTTCCTTAAGCAT 26
 | | | | | | | | | | | | | |
pb 7141 CAACCTCCACTCCCTTCCTTAAGCAT 7116

RESULT 5
 US-10-424-599-7186
 ; Sequence 7186, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 7186
 ; LENGTH: 796
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_106497C.1
 US-10-424-599-7186

Query Match 72.3%; Score 18.8; DB 7; Length 796;
Best Local Similarity 90.9%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACCTCATGCCCTTCCTAA 22
Db 731 CCACCTCATGCCACTTCCAA 752

RESULT 6
US-09-925-065A-49324/c
; Sequence 49324, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30

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; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49324
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-49324

```

Query Match	70.0%;	Score 18.2;	DB 4;	Length 537;
Best Local Similarity	87.0%;	Pred. NO. 1.9e+02;		
Matches 20; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 CACCTCATCGCCCCCTTCCCTAAGC 24
|||
Db 124 CACCTCCTCGCCCCCTCCTCAGC 102

RESULT 7

US-09-925-065A-49325/c

; Sequence 49325, Application US/09925065A

; Publication No. US20050228172A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

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Query Match          70.0%; Score 18.2; DB 4; Length 537;
Best Local Similarity 87.0%; Pred. NO. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 2 CACCTCATCGCCCCCTTCTAAGC 24
|||
Db 124 CACCTCTCGCCCCCTTCTCAGC 102

RESULT 8
US-09-925-065A-262314
; Sequence 262314, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147

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; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262314
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-262314

```

Query Match 70.0%; Score 18.2; DB 4; Length 569;
Best Local Similarity 87.0%;
Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	2	CACCTCATCGCCCCCTTCTAAGC	24
Dδ	495	CACCTCTCGCCCCCTCCTCAGC	517

RESULT 9
US-09-925-065A-437738
; Sequence 437738, Application US/09925065A
; Publication No. US20050228172A9

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Query Match          70.0%; Score 18.2; DB 4; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 2 CACCTCATCGCCCCCTTCTAAGC 24
Dbb 495 CACCTCTCGCCCCCTCTCAGC 517

RESULT 10
 US-09-925-065A-437739
 ; Sequence 437739, Application US/09925065A
 ; Publication No. US20050228172A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08


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; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 437739
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437739

Query Match          70.0%; Score 18.2; DB 4; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CACCTCATCGCCCTTCCTAAGC 24
        ||||| ||||| ||||| ||||| |||||
Db      495 CACCTCCTCGCCCTCCTCAGC 517

RESULT 11
US-09-925-065A-437740
; Sequence 437740, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 437740
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437740

Query Match          70.0%; Score 18.2; DB 4; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CACCTCATCGCCCTTCCTAAGC 24
        ||||| ||||| ||||| ||||| |||||
Db      495 CACCTCCTCGCCCTCCTCAGC 517

RESULT 12
US-09-764-877-2860
; Sequence 2860, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
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; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2860
; LENGTH: 5549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2860

Query Match          70.0%; Score 18.2; DB 3; Length 5549;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CACCTCATCGCCCTTCCTAAGC 24
        ||||| ||||| ||||| ||||| |||||
Db      2510 CACCTCCTCGCCCTCCTCAGC 2532

RESULT 13
US-10-242-515-2860
; Sequence 2860, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2860
; LENGTH: 5549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-2860

Query Match          70.0%; Score 18.2; DB 6; Length 5549;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  CACCTCATCGCCCTTCCTAAGC 24
        ||||| ||||| ||||| ||||| |||||
Db      2510 CACCTCCTCGCCCTCCTCAGC 2532

RESULT 14
US-10-087-192-1690
; Sequence 1690, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
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; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1690
; LENGTH: 58952
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(58952)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1690

Query Match 70.0%; Score 18.2; DB 5; Length 58952;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCCTAAG 23
|||||
Db 30297 CCACCCCATCTCCCTTCCTAAG 30319

RESULT 15
US-09-820-007-3
; Sequence 3, Application US/09820007
; Publication No. US20040229304A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001205
; CURRENT APPLICATION NUMBER: US/09/820,007
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 213456
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(213456)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-007-3

Query Match 70.0%; Score 18.2; DB 3; Length 213456;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCTTCCTAAGCAT 26
|||||
Db 184770 CCTCATCACTCCTTCCAAAGCAT 184792

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OM nucleic - nucleic search, using sw model

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Title: US-09-904-968A-4
Perfect score: 26
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /SID55/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /SID55/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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- 8: /SID55/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
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- 12: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
- 13: /SID55/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
- 14: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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- 18: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
- 19: /SID55/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	19.2	73.8	1872	11 US-10-932-182A-3010	Sequence 3010, Ap
2	19.2	73.8	1872	11 US-10-932-182A-3010	Sequence 3010, Ap
3	19.2	73.8	90739	11 US-10-330-773-902	Sequence 902, App
C 4	18.2	70.0	537	7 US-09-925-065A-49324	Sequence 49324, A
C 5	18.2	70.0	537	7 US-09-925-065A-49325	Sequence 49325, A
C 6	18.2	70.0	537	11 US-10-301-480-150562	Sequence 150562,
C 7	18.2	70.0	537	11 US-10-301-480-150563	Sequence 150563,
C 8	18.2	70.0	537	12 US-10-301-480-763971	Sequence 763971,
C 9	18.2	70.0	537	12 US-10-301-480-763972	Sequence 763972,
10	18.2	70.0	569	7 US-09-925-065A-262314	Sequence 262314,
11	18.2	70.0	569	7 US-09-925-065A-437738	Sequence 437738,
12	18.2	70.0	569	7 US-09-925-065A-437739	Sequence 437739,
13	18.2	70.0	569	7 US-09-925-065A-437740	Sequence 437740,
14	18.2	70.0	572	12 US-10-301-480-340535	Sequence 340535,

15	18.2	70.0	572	12	US-10-301-480-499114	Sequence 499114,
16	18.2	70.0	572	12	US-10-301-480-499115	Sequence 499115,
17	18.2	70.0	572	12	US-10-301-480-953944	Sequence 953944,
18	18.2	70.0	572	12	US-10-301-480-1112523	Sequence 1112523,
19	18.2	70.0	572	12	US-10-301-480-1112524	Sequence 1112524,
C 20	18	69.2	575	7	US-09-925-065A-471791	Sequence 471791,
21	18	69.2	1068	10	US-10-750-185-39158	Sequence 39158, A
22	18	69.2	1068	10	US-10-750-623-39158	Sequence 39158, A
C 23	18	69.2	1673	10	US-10-750-185-47820	Sequence 47820, A
C 24	18	69.2	1673	10	US-10-750-623-47820	Sequence 47820, A
C 25	17.8	68.5	537	7	US-09-925-065A-49323	Sequence 49323, A
C 26	17.8	68.5	537	11	US-10-301-480-150561	Sequence 150561,
C 27	17.8	68.5	537	12	US-10-301-480-763970	Sequence 763970,
28	17.8	68.5	567	7	US-09-925-065A-590403	Sequence 590403,
29	17.8	68.5	569	7	US-09-925-065A-437741	Sequence 437741,
30	17.8	68.5	572	12	US-10-301-480-499116	Sequence 499116,
31	17.8	68.5	572	12	US-10-301-480-1112525	Sequence 1112525,
32	17.6	67.7	675	7	US-09-925-065A-502013	Sequence 502013,
C 33	17.6	67.7	3022	10	US-10-750-185-42216	Sequence 42216, A
C 34	17.6	67.7	3022	10	US-10-750-623-42216	Sequence 42216, A
C 35	17.6	67.7	11282	17	US-11-177-504-1	Sequence 1, Appli
36	17.6	67.7	23704	17	US-11-124-368A-2905	Sequence 2905, Ap
C 37	17.6	67.7	268685	10	US-10-933-025-22	Sequence 22, Appl
C 38	17.6	67.7	268685	18	US-11-219-360-22	Sequence 22, Appl
C 39	17.2	66.2	459	7	US-09-925-065A-447393	Sequence 447393,
C 40	17.2	66.2	2937	10	US-10-750-185-60052	Sequence 60052, A
C 41	17.2	66.2	2937	10	US-10-750-623-60052	Sequence 60052, A
C 42	17	65.4	390	9	US-10-511-937-552	Sequence 552, App
C 43	17	65.4	457	12	US-10-301-480-379405	Sequence 379405,
C 44	17	65.4	457	12	US-10-301-480-992814	Sequence 992814,
C 45	17	65.4	458	7	US-09-925-065A-303251	Sequence 303251,

ALIGNMENTS

RESULT 1
US-10-932-182A-3010
; Sequence 3010, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3010

Query Match 73.8%; Score 19.2; DB 11; Length 1872;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCACCTCATCGCCCTTCCTAAGC 24
| | | | | | | | | | | | | | | | | | | | | |
Db 664 CCACCTCATGGCCCTTCCCAACC 687

RESULT 2
US-10-932-182A-3010
; Sequence 3010, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO

```
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3010

Query Match          73.8%; Score 19.2; DB 11; Length 1872;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCCTAAGC 24
||||||| ||||||| |||

Db 664 CCACCTCATGCGCCCTTCCCAACC 687

RESULT 3
US-10-330-773-902
; Sequence 902, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 902
; LENGTH: 90739
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(90739)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-902

Query Match          73.8%; Score 19.2; DB 11; Length 90739;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCTTCCTAAGCAT 26
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Db 68646 ACCTCATCACCCTTCCTCTGCAT 68669

RESULT 4
US-09-925-065A-49324/c
; Sequence 49324, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
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; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49324
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-49324

Query Match          70.0%; Score 18.2; DB 7; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 124 CACCTCCTCGCCCTCCTCAGC 102

RESULT 5
US-09-925-065A-49325/c
; Sequence 49325, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49325
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-49325

Query Match          70.0%; Score 18.2; DB 7; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 124 CACCTCCTCGCCCTCCTCAGC 102

RESULT 6
US-10-301-480-150562/c
; Sequence 150562, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
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; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150562
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-150562

Query Match 70.0%; Score 18.2; DB 11; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 124 CACCTCCTCGCCCCCTCCTCAGC 102

RESULT 7
US-10-301-480-150563/c
; Sequence 150563, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150563
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-150563

Query Match 70.0%; Score 18.2; DB 11; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 124 CACCTCCTCGCCCCCTCCTCAGC 102

RESULT 8
US-10-301-480-763971/c
; Sequence 763971, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 763971
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-763971

Query Match 70.0%; Score 18.2; DB 12; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 124 CACCTCCTCGCCCCCTCCTCAGC 102

RESULT 9
US-10-301-480-763972/c
; Sequence 763972, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 763972
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-763972

Query Match 70.0%; Score 18.2; DB 12; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 124 CACCTCCTCGCCCCCTCCTCAGC 102

RESULT 10
US-09-925-065A-262314
; Sequence 262314, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 262314
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-262314

Query Match 70.0%; Score 18.2; DB 7; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| |||||
Db 495 CACCTCCTCGCCCCCTCCTCAGC 517

RESULT 11
US-09-925-065A-437738
; Sequence 437738, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437738
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437738

Query Match 70.0%; Score 18.2; DB 7; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| |||||
Db 495 CACCTCCTCGCCCCCTCCTCAGC 517

RESULT 12
US-09-925-065A-437739
; Sequence 437739, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437739
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437739

Query Match 70.0%; Score 18.2; DB 7; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| |||||
Db 495 CACCTCCTCGCCCCCTCCTCAGC 517

RESULT 13
US-09-925-065A-437740
; Sequence 437740, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437740
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437740

Query Match 70.0%; Score 18.2; DB 7; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| |||||
Db 495 CACCTCCTCGCCCCCTCCTCAGC 517

RESULT 14
US-10-301-480-340535
; Sequence 340535, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340535
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-340535

Query Match 70.0%; Score 18.2; DB 12; Length 572;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
|||||
Db 495 CACCTCTCGCCCTCCTCAGC 517

RESULT 15
US-10-301-480-499114
; Sequence 499114, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 499114
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-499114

Query Match 70.0%; Score 18.2; DB 12; Length 572;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
|||||
Db 495 CACCTCTCGCCCTCCTCAGC 517

Search completed: May 9, 2006, 06:39:10
Job time : 589.178 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:14:10 ; Search time 52.3556 Seconds
(without alignments)
645.083 Million cell updates/sec

Title: US-09-904-968A-19

Perfect score: 19

Sequence: 1 ggctgcgctgtggcgaagg 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCUTUS_COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	100.0	31571	2	US-08-323-443B-1
2	19	100.0	53526	3	US-08-658-136-2
3	19	100.0	53577	3	US-08-658-136-1
4	19	100.0	53577	3	US-08-460-215A-1
5	16.4	86.3	906	3	US-09-489-039A-565
C 6	16.4	86.3	954	3	US-09-489-039A-449
7	15.8	83.2	780	3	US-09-902-540-5800
C 8	15.8	83.2	858	3	US-09-902-540-8298
9	15.8	83.2	6935	3	US-09-902-540-865
10	15.8	83.2	72704	3	US-09-902-540-1273
C 11	15.4	81.1	1182	3	US-09-902-540-8004
12	15.4	81.1	6439	3	US-09-902-540-813
13	15	78.9	633	3	US-08-998-416-1115
14	15	78.9	1173	3	US-09-489-039A-1206
C 15	15	78.9	3396	3	US-09-668-680-6
C 16	15	78.9	3423	3	US-09-668-680-7
17	14.8	77.9	150	3	US-09-513-999C-32794
18	14.8	77.9	153	3	US-09-471-276-696
C 19	14.8	77.9	278	3	US-09-313-294A-2721
20	14.8	77.9	435	3	US-09-902-540-8251
C 21	14.8	77.9	601	3	US-09-949-016-139687
C 22	14.8	77.9	601	3	US-09-949-016-139688
C 23	14.8	77.9	1155	3	US-09-902-540-7960
24	14.8	77.9	1179	3	US-09-902-540-8018

25	14.8	77.9	2502	3	US-09-902-540-4680	Sequence 4680, Ap
C 26	14.8	77.9	2598	3	US-09-252-991A-2768	Sequence 2768, Ap
C 27	14.8	77.9	2643	3	US-09-614-221A-287	Sequence 287, App
C 28	14.8	77.9	2643	3	US-09-487-558B-439	Sequence 439, App
C 29	14.8	77.9	2790	3	US-09-252-991A-2864	Sequence 2864, Ap
30	14.8	77.9	6134	3	US-09-902-540-805	Sequence 805, App
31	14.8	77.9	6492	3	US-09-902-540-853	Sequence 853, App
C 32	14.8	77.9	9053	3	US-09-902-540-815	Sequence 815, App
C 33	14.8	77.9	24754	3	US-09-902-540-1230	Sequence 1230, Ap
34	14.8	77.9	28509	3	US-09-902-540-1240	Sequence 1240, Ap
35	14.8	77.9	87039	3	US-09-949-016-15691	Sequence 15691, A
36	14.4	75.8	317	3	US-09-221-017B-595	Sequence 595, App
C 37	14.4	75.8	1830	3	US-08-969-683A-66	Sequence 66, Appl
C 38	14.4	75.8	1830	3	US-09-308-207-66	Sequence 66, Appl
C 39	14.4	75.8	1860	3	US-09-489-039A-3038	Sequence 3038, Ap
C 40	14.4	75.8	2812	3	US-09-620-312D-624	Sequence 624, App
41	14.4	75.8	3405	3	US-09-614-221A-425	Sequence 425, App
42	14.4	75.8	4430	3	US-09-902-540-491	Sequence 491, Appl
43	14.4	75.8	15872	3	US-09-105-537-1	Sequence 1, Appli
44	14.4	75.8	15872	3	US-09-091-609-1	Sequence 1, Appli
45	14.4	75.8	15872	3	US-09-091-609-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-323-443B-1/c
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/0A462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens


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; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match      100.0%; Score 19; DB 2; Length 31571;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
Db 3599 GGTCGCGCTGTGGCGAAGG 3581

RESULT 2
US-08-658-136-2
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match      100.0%; Score 19; DB 3; Length 53526;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
Db 3334 GGTCGCGCTGTGGCGAAGG 3352

RESULT 3
US-08-658-136-1
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match      100.0%; Score 19; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
Db 3334 GGTCGCGCTGTGGCGAAGG 3352

RESULT 4
US-08-460-215A-1
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,215A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUGAN, DEBORAH
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-17.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-460-215A-1

Query Match 100.0%; Score 19; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGGCGAAGG 19
|||||
Db 3334 GGTCGGCGCTGTGGCGAAGG 3352

RESULT 5

US-09-489-039A-565
; Sequence 565, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 565
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-565

Query Match 86.3%; Score 16.4; DB 3; Length 906;
Best Local Similarity 94.4%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGGCGAAG 18
|||||
Db 218 GGTCGGCGCTGTGGCGAAG 235

RESULT 6

US-09-489-039A-449/c
; Sequence 449, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 449
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-449

Query Match 86.3%; Score 16.4; DB 3; Length 954;
Best Local Similarity 94.4%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGGCGAAG 18
|||||
Db 725 GGTCGGCGCTGTGGCGAAG 708

RESULT 7

US-09-902-540-5800
; Sequence 5800, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5800
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5800

Query Match 83.2%; Score 15.8; DB 3; Length 780;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGGCGAAGG 19
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Db 55 GGTCGGCGGTGGCGGAGG 73

RESULT 8

US-09-902-540-8298/c
; Sequence 8298, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8298
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8298

Query Match 83.2%; Score 15.8; DB 3; Length 858;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
| | | | | | | | | | | | | | | | | | | |
Db 844 GGTCGCGCTGTGGCGGAGG 826

RESULT 9
US-09-902-540-865
; Sequence 865, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 865
; LENGTH: 6935
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-865

Query Match 83.2%; Score 15.8; DB 3; Length 6935;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
| | | | | | | | | | | | | | | | | | | |
Db 16 GGTCGCGCTGGGCGGAGG 34

RESULT 10
US-09-902-540-1273
; Sequence 1273, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1273
; LENGTH: 72704
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72704)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273

Query Match 83.2%; Score 15.8; DB 3; Length 72704;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
| | | | | | | | | | | | | | | | | | | |
Db 65126 GGTCGCGCGTGGCGGAGG 65144

RESULT 11

US-09-902-540-8004/c
; Sequence 8004, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8004
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8004

Query Match 81.1%; Score 15.4; DB 3; Length 1182;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCGCGCTGTGGCGAAGG 19
| | | | | | | | | | | | | | | | | | | |
Db 336 TCGCGCTTGGCGAAGG 320

RESULT 12
US-09-902-540-813
; Sequence 813, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 813
; LENGTH: 6439
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-813

Query Match 81.1%; Score 15.4; DB 3; Length 6439;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCGCGCTGTGGCGAAGG 19
| | | | | | | | | | | | | | | | | | | |
Db 849 TCGCGCTTGGCGAAGG 865

RESULT 13
US-08-998-416-1115
; Sequence 1115, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jorgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne

Query Match 78.9%; Score 15; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels

Search completed: May 9, 2006, 05:56:09
Job time : 53.3556 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:26:49 ; Search time 460.011 Seconds
(without alignments)
341.553 Million cell updates/sec

Title: US-09-904-968A-19
Perfect score: 19
Sequence: 1 ggctgcgctgtggcgaagg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	3	US-09-904-968A-19
2	19	100.0	53522	3	US-09-904-968A-1
3	17.4	91.6	623	8	US-10-363-345A-2649
4	17.4	91.6	623	8	US-10-363-345A-2650
5	17.4	91.6	623	9	US-10-363-483A-2649
6	17.4	91.6	623	9	US-10-363-483A-2650
7	17.4	91.6	6423	6	US-10-240-485-121
8	16.4	86.3	871	7	US-10-437-963-87337
9	15.8	83.2	656	7	US-10-437-963-31042
10	15.8	83.2	762	6	US-10-369-493-43242
11	15.8	83.2	1059	10	US-11-109-593-15
12	15.8	83.2	2047	8	US-10-425-115-137211
13	15.8	83.2	5373	10	US-11-097-143-7789
14	15.8	83.2	67323	10	US-11-109-593-1
15	15.8	83.2	155350	7	US-10-322-281-691
16	15.4	81.1	447	7	US-10-437-963-19948
17	15.4	81.1	479	7	US-10-767-701-22213
18	15.4	81.1	1176	6	US-10-369-493-42897
19	15.4	81.1	1518	5	US-10-116-821-13
20	15.4	81.1	1518	5	US-10-117-283-13
21	15.4	81.1	1627	7	US-10-425-114-20510
22	15.4	81.1	2386	8	US-10-425-115-120685
23	15.4	81.1	2619	3	US-09-789-561-80

24	15.4	81.1	2619	8	US-10-883-936-80	Sequence 80, Appl
25	15	78.9	609	8	US-10-425-115-153994	Sequence 153994,
26	15	78.9	921	7	US-10-282-122A-13107	Sequence 13107, A
27	15	78.9	1106	7	US-10-767-701-12786	Sequence 12786, A
28	15	78.9	1840	9	US-10-450-763-1347	Sequence 1347, Ap
29	15	78.9	2130	9	US-10-450-763-8547	Sequence 8547, Ap
30	15	78.9	2280	9	US-10-450-763-25859	Sequence 25859, A
31	15	78.9	2280	9	US-10-450-763-29784	Sequence 29784, A
32	15	78.9	2301	9	US-10-450-763-5882	Sequence 5882, Ap
33	15	78.9	3236	7	US-10-191-803-219	Sequence 219, App
34	15	78.9	3236	7	US-10-205-331-11	Sequence 11, Appl
35	15	78.9	3236	7	US-10-152-319A-1951	Sequence 1951, Ap
36	15	78.9	3384	6	US-10-240-145-92	Sequence 92, Appl
37	15	78.9	3384	9	US-10-450-763-13434	Sequence 13434, A
38	15	78.9	3384	9	US-10-450-763-24535	Sequence 24535, A
39	15	78.9	3384	9	US-10-291-128-92	Sequence 92, Appl
40	15	78.9	3396	5	US-10-146-419-6	Sequence 6, Appli
41	15	78.9	3396	5	US-10-146-123-6	Sequence 6, Appli
42	15	78.9	3423	5	US-10-146-419-7	Sequence 7, Appli
43	15	78.9	3423	5	US-10-146-123-7	Sequence 7, Appli
44	15	78.9	3515	7	US-10-276-774-851	Sequence 851, App
45	15	78.9	3532	9	US-10-956-157-1857	Sequence 1857, Ap

ALIGNMENTS

RESULT 1
US-09-904-968A-19
; Sequence 19, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer 1F1
US-09-904-968A-19

Query Match 100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
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Db 1 GGTCGCGCTGTGGCGAAGG 19

RESULT 2
US-09-904-968A-1
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE

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; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 53522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-968A-1

Query Match          100.0%; Score 19; DB 3; Length 53522;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGGCGAAGG 19
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Db 3334 GGTCGCGCTGTGGCGAAGG 3352

RESULT 3
US-10-363-345A-2649
; Sequence 2649, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2649
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-2649

Query Match          91.6%; Score 17.4; DB 8; Length 623;
Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGGCGAAGG 19
   |||||
Db 196 GGTCGCGTGTGGCGAAGG 214

RESULT 4
US-10-363-345A-2650/c
; Sequence 2650, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2650
; LENGTH: 623
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-2650

Query Match          91.6%; Score 17.4; DB 8; Length 623;
Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGGCGAAGG 19
   |||||
Db 428 GGTCGCGTGTGGCGAAGG 410

RESULT 5
US-10-363-483A-2649
; Sequence 2649, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2649
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-2649

Query Match          91.6%; Score 17.4; DB 9; Length 623;
Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGGCGAAGG 19
   |||||
Db 196 GGTCGCGTGTGGCGAAGG 214

RESULT 6
US-10-363-483A-2650/c
; Sequence 2650, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2650
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-2650

Query Match          91.6%; Score 17.4; DB 9; Length 623;
Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GGTCGCGCTGTGGCGAAGG 19
|||||
Db 428 GGTCGCGTGTGGCGAAGG 410

RESULT 7
US-10-240-485-121
; Sequence 121, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 121
; LENGTH: 6423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-121

Query Match 91.6%; Score 17.4; DB 6; Length 6423;
Best Local Similarity 94.7%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
|||||
Db 4895 GGTCGCGTGTGGCGAAGG 4913

RESULT 8
US-10-437-963-87337
; Sequence 87337, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 87337
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_86292C.1
US-10-437-963-87337

Query Match 86.3%; Score 16.4; DB 7; Length 871;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCGCGCTGTGGCGAAGG 19
|||||
Db 465 GTCGCGCGTGTGGCGAAGG 482

RESULT 9
US-10-437-963-31042
; Sequence 31042, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 31042
; LENGTH: 656
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35387C.1
US-10-437-963-31042

Query Match 83.2%; Score 15.8; DB 7; Length 656;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTGCGCGCTGTGGCGAAGG 19
|||||
Db 625 GGCCGCGCTGTGGCGACGG 643

RESULT 10
US-10-369-493-43242
; Sequence 43242, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 43242
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-10-369-493-43242

Query Match 83.2%; Score 15.8; DB 6; Length 762;
Best Local Similarity 89.5%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
|||||
Db 55 GGTCGCGCGTGGCGGAGG 73

RESULT 11
US-11-109-593-15
; Sequence 15, Application US/11109593
; Publication No. US20050233369A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Ralph
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR JERANGOLIDS
; FILE REFERENCE: 010108.01
; CURRENT APPLICATION NUMBER: US/11/109,593
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,843
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-109-593-15

Query Match 83.2%; Score 15.8; DB 10; Length 1059;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
|||||
Db 652 GGTCGCGCGTGGCGGAGG 670

RESULT 12
US-10-425-115-137211/c
; Sequence 137211, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 137211
; LENGTH: 2047
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_56611C.1
US-10-425-115-137211

Query Match 83.2%; Score 15.8; DB 8; Length 2047;
Best Local Similarity 89.5%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
|||||
Db 307 GGTCGCGCAGGGCGAAGG 289

RESULT 13
US-11-097-143-7789/c
; Sequence 7789, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7789
; LENGTH: 5373
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-7789

Query Match 83.2%; Score 15.8; DB 10; Length 5373;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
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Db 3054 GGACTCGCTGTGGCGAAGG 3036

RESULT 14
US-11-109-593-1
; Sequence 1, Application US/11109593
; Publication No. US20050233369A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Ralph
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR JERANGOLIDS
; FILE REFERENCE: 010108.01
; CURRENT APPLICATION NUMBER: US/11/109,593
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,843
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 67323
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-109-593-1

Query Match 83.2%; Score 15.8; DB 10; Length 67323;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGAAGG 19
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Db 56836 GGTCGCGCGTGGCGGAGG 56854

RESULT 15
US-10-322-281-691

; Sequence 691, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 691
; LENGTH: 155350
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(155350)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-691

Query Match 83.2%; Score 15.8; DB 7; Length 155350;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGCGAAGG 19
||| ||||| ||||| |||||
Db 10227 GGGCGGCGCTGTGCGGAGG 10245

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OM nucleic - nucleic search, using sw model

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(without alignments)
180.024 Million cell updates/sec

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Sequence: 1 ggtcgcgtgtggcgaagg 19

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Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /SID55/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /SID55/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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17: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
18: /SID55/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
19: /SID55/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	19	100.0	977	12	US-10-301-480-570506 Sequence 570506,
2	19	100.0	977	12	US-10-301-480-1183915 Sequence 1183915,
3	17.4	91.6	975	12	US-10-301-480-576105 Sequence 576105,
4	17.4	91.6	975	12	US-10-301-480-1189514 Sequence 1189514,
C 5	15.8	83.2	36360	10	US-10-995-561-13498 Sequence 13498, A
6	15.4	81.1	1518	18	US-11-282-000-13 Sequence 13, Appl
C 7	15	78.9	3236	18	US-11-036-196-1951 Sequence 1951, Ap
C 8	15	78.9	3581	17	US-11-136-527-3057 Sequence 3057, Ap
C 9	14.8	77.9	828	11	US-10-932-182A-80342 Sequence 80342, A
C 10	14.8	77.9	828	11	US-10-932-182A-80342 Sequence 80342, A
C 11	14.8	77.9	1455	11	US-10-932-182A-80341 Sequence 80341, A
C 12	14.8	77.9	1455	11	US-10-932-182A-80341 Sequence 80341, A
C 13	14.8	77.9	1614	18	US-11-096-568A-19074 Sequence 19074, A
14	14.4	75.8	3405	11	US-10-932-182A-77844 Sequence 77844, A

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C 16	14.4	75.8	162289	17	US-11-121-086-20	Sequence 20, Appl
C 17	14.2	74.7	21	10	US-10-310-914A-107405	Sequence 107405,
18	14.2	74.7	25	11	US-10-933-982-216667	Sequence 216667,
19	14.2	74.7	379	10	US-10-527-500-76	Sequence 76, Appl
20	14.2	74.7	497	12	US-10-301-480-467810	Sequence 467810,
21	14.2	74.7	497	12	US-10-301-480-1081219	Sequence 1081219,
22	14.2	74.7	500	7	US-09-925-065A-400591	Sequence 400591,
C 23	14.2	74.7	531	7	US-09-925-065A-829581	Sequence 829581,
24	14.2	74.7	532	7	US-09-925-065A-759970	Sequence 759970,
C 25	14.2	74.7	538	7	US-09-925-065A-822760	Sequence 822760,
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27	14.2	74.7	564	7	US-09-925-065A-882340	Sequence 882340,
C 28	14.2	74.7	574	7	US-09-925-065A-545421	Sequence 545421,
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C 30	14.2	74.7	582	7	US-09-925-065A-802642	Sequence 802642,
C 31	14.2	74.7	591	7	US-09-925-065A-806815	Sequence 806815,
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C 33	14.2	74.7	592	11	US-10-301-480-154036	Sequence 154036,
C 34	14.2	74.7	592	12	US-10-301-480-767445	Sequence 767445,
C 35	14.2	74.7	597	7	US-09-925-065A-802303	Sequence 802303,
C 36	14.2	74.7	597	7	US-09-925-065A-802401	Sequence 802401,
C 37	14.2	74.7	597	7	US-09-925-065A-802539	Sequence 802539,
38	14.2	74.7	598	7	US-09-925-065A-495552	Sequence 495552,
C 39	14.2	74.7	600	17	US-11-136-527-6618	Sequence 6618, Ap
C 40	14.2	74.7	702	7	US-09-925-065A-698630	Sequence 698630,
C 41	14.2	74.7	702	7	US-09-925-065A-698631	Sequence 698631,
C 42	14.2	74.7	714	11	US-10-301-480-100859	Sequence 100859,
C 43	14.2	74.7	714	12	US-10-301-480-714268	Sequence 714268,
C 44	14.2	74.7	875	18	US-11-096-568A-10111	Sequence 10111, A
C 45	14.2	74.7	928	18	US-11-096-568A-18550	Sequence 18550, A

ALIGNMENTS

RESULT 1
US-10-301-480-570506
; Sequence 570506, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 570506
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-570506

Query Match 100.0%; Score 19; DB 12; Length 977;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGTCGCGCTGTGGCGAAGG 19
|||||
Db 13 GGTCGCGCTGTGGCGAAGG 31

RESULT 2
US-10-301-480-1183915
; Sequence 1183915, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1183915
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1183915

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```
Query Match      100.0%; Score 19; DB 12; Length 977;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGTGGCGCTGTGGCGAAGG 19
|||
Db 13 GGTGGCGCTGTGGCGAAGG 31

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RESULT 3
US-10-301-480-576105
; Sequence 576105, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 576105
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57, 206
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-576105

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Query Match          91.6%; Score 17.4; DB 12; Length 975;
Best Local Similarity 94.7%; Pred. NO. 15;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GGTGCGCTGTGGCAAGG 19
|||
Db 6 GGTGCGCTGTGGCAACG 24

RESULT 4
US-10-301-480-1189514
; Sequence 1189514, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480

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; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1189514
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57, 206
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-1189514

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Query Match	91.6%;	Score 17.4;	DB 12;	Length 975;
Best Local Similarity	94.7%;	Pred. No. 15;		
Matches 18; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;

Qy 1 GGTCCGCTGTGGCGAAGG 19
|||
db 6 GGTCCGCTGTGGCGAAGG 24

RESULT 5
 US-10-995-561-13498/c
 ; Sequence 13498, Application US/10995561
 ; Publication No. US20050272054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 ; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001559
 ; CURRENT APPLICATION NUMBER: US/10/995,561
 ; CURRENT FILING DATE: 2004-11-24
 ; NUMBER OF SEQ ID NOS: 85702
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 13498
 ; LENGTH: 36360
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-995-561-13498

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Query Match      83.2%; Score 15.8; DB 10; Length 36360;
Best Local Similarity 89.5%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 GGTCGCGCTGTGGCGAAGG 19
24538 GGGCGGGCTGTGGCGAAGG 24520
db

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RESULT 6
US-11-282-000-13
; Sequence 13, Application US/11282000
; Publication No. US20060068477A1
; GENERAL INFORMATION:
; APPLICANT: Dodge, Timothy C.
; APPLICANT: Valle, Fernando
; TITLE OF INVENTION: Methods for the Production of Products
; TITLE OF INVENTION: in Host Cells
; FILE REFERENCE: GC620-3
; CURRENT APPLICATION NUMBER: US/11/282,000
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 10/116,821
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,277
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 13
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Pantoea citrea
US-11-282-000-13

Query Match      81.1%; Score 15.4; DB 18; Length 1518;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTGCGCTGTGGCGAA 17
      ||| ||||| ||||| |||||
Db      1237 GGTGCGCTGTGGCGAA 1253

RESULT 7
US-11-036-196-1951/c
; Sequence 1951, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; PRIOR FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1951
; LENGTH: 3236
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_031814
US-11-036-196-1951

Query Match      78.9%; Score 15; DB 18; Length 3236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCGCTGTGGCGAAGG 19
      ||||| ||||| |||||
Db      216 GCGCTGTGGCGAAGG 202

RESULT 8
US-11-136-527-3057/c
; Sequence 3057, Application US/11136527
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; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3057
; LENGTH: 3581
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3057

Query Match      78.9%; Score 15; DB 17; Length 3581;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCGCTGTGGCGAAGG 19
      ||||| ||||| |||||
Db      216 GCGCTGTGGCGAAGG 202

RESULT 9
US-10-932-182A-80342/c
; Sequence 80342, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80342
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80342

Query Match      77.9%; Score 14.8; DB 11; Length 828;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GTCGCGCTGTGGCGAAGG 19
      | ||||| ||||| |||||
Db      182 GCGCGCTGTGGTGAAGG 165

RESULT 10
US-10-932-182A-80342/c
; Sequence 80342, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80342
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80342

Query Match          77.9%; Score 14.8; DB 11; Length 828;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GTCGCGCTGTGGCGAAGG 19
      | ||||| ||||| |||||
Db      182  GGCGCGCTGTGGTGAAGG 165

RESULT 11
US-10-932-182A-80341/c
; Sequence 80341, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80341
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80341

Query Match          77.9%; Score 14.8; DB 11; Length 1455;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GTCGCGCTGTGGCGAAGG 19
      | ||||| ||||| |||||
Db      182  GGCGCGCTGTGGTGAAGG 165

RESULT 12
US-10-932-182A-80341/c
; Sequence 80341, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80341
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80341

Query Match          77.9%; Score 14.8; DB 11; Length 1455;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GTCGCGCTGTGGCGAAGG 19
      | ||||| ||||| |||||
Db      182  GGCGCGCTGTGGTGAAGG 165

RESULT 13
US-11-096-568A-19074
; Sequence 19074, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19074
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1614)
; OTHER INFORMATION: Ceres Seq. ID no. 12368767
US-11-096-568A-19074

Query Match          77.9%; Score 14.8; DB 18; Length 1614;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GGTCGCGCTGTGGCGAAG 18
      | ||||| ||||| |||||
Db      383  GATCGCGCTGTGGCAAAG 400

RESULT 14
US-10-932-182A-77844
; Sequence 77844, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77844
; LENGTH: 3405
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77844

Query Match          75.8%; Score 14.4; DB 11; Length 3405;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GGTCGCGCTGTGGCGA 16
      ||||| ||||| |||||
Db      2878  GGTCGCGCTGTGGCGA 2893

RESULT 15
US-10-932-182A-77844
; Sequence 77844, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80342
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80342

Query Match          77.9%; Score 14.8; DB 11; Length 828;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GTCGCGCTGTGGCGAAGG 19
      | ||||| ||||| |||||
Db      182  GGCGCGCTGTGGTGAAGG 165

RESULT 13
US-11-096-568A-19074
; Sequence 19074, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19074
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1614)
; OTHER INFORMATION: Ceres Seq. ID no. 12368767
US-11-096-568A-19074

Query Match          77.9%; Score 14.8; DB 18; Length 1614;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GGTCGCGCTGTGGCGAAG 18
      | ||||| ||||| |||||
Db      383  GATCGCGCTGTGGCAAAG 400

RESULT 14
US-10-932-182A-77844
; Sequence 77844, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77844
; LENGTH: 3405
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77844

Query Match          75.8%; Score 14.4; DB 11; Length 3405;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GGTCGCGCTGTGGCGA 16
      ||||| ||||| |||||
Db      2878  GGTCGCGCTGTGGCGA 2893

RESULT 15
US-10-932-182A-77844
; Sequence 77844, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
```


; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77844
; LENGTH: 3405
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77844

Query Match 75.8%; Score 14.4; DB 11; Length 3405;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCGCGCTGTGGCGA 16
||| |||||
Db 2878 GGTCGCGCTGTGGCGA 2893

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Job time : 429.822 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:14:10 ; Search time 44.0889 Seconds
(without alignments)
645.083 Million cell updates/sec

Title: US-09-904-968A-20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

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3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
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9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	16	100.0	30	3	US-09-052-469-15
2	16	100.0	30	3	US-08-422-582-15
3	16	100.0	30	3	US-09-052-262-15
4	16	100.0	1281	3	US-09-902-540-2359
C 5	16	100.0	13941	3	US-09-799-451-341
C 6	16	100.0	14060	3	US-08-658-136-4
C 7	16	100.0	14136	3	US-10-083-246A-1
C 8	16	100.0	14148	3	US-09-052-469-7
C 9	16	100.0	14148	3	US-08-422-582-7
C 10	16	100.0	14148	3	US-09-052-262-7
C 11	16	100.0	15447	3	US-09-902-540-1100
C 12	16	100.0	31571	2	US-08-323-443B-1
C 13	16	100.0	53526	3	US-08-658-136-2
C 14	16	100.0	53577	3	US-08-658-136-1
C 15	16	100.0	53577	3	US-08-460-215A-1
16	15	93.8	30	3	US-09-052-469-16
17	15	93.8	30	3	US-08-422-582-16
18	15	93.8	30	3	US-09-052-262-16
C 19	15	93.8	511	3	US-10-324-316-25
C 20	15	93.8	996	3	US-09-252-991A-2201
C 21	15	93.8	1530	3	US-09-902-540-4366
C 22	15	93.8	1641	3	US-09-252-991A-2551
C 23	15	93.8	1791	3	US-09-252-991A-2363
C 24	15	93.8	3135	3	US-09-252-991A-2282

25	15	93.8	23694	3	US-09-902-540-1216	Sequence 1216, Ap
26	14.4	90.0	354	3	US-09-489-039A-1395	Sequence 1395, Ap
27	14.4	90.0	357	3	US-09-252-991A-15903	Sequence 15903, A
28	14.4	90.0	435	3	US-09-902-540-8251	Sequence 8251, Ap
C 29	14.4	90.0	594	3	US-09-902-540-3456	Sequence 3456, Ap
C 30	14.4	90.0	688	2	US-08-840-683-2	Sequence 2, Appli
C 31	14.4	90.0	688	2	US-08-555-722-2	Sequence 2, Appli
C 32	14.4	90.0	688	3	US-09-384-301-2	Sequence 2, Appli
C 33	14.4	90.0	759	3	US-09-303-518D-297	Sequence 297, App
C 34	14.4	90.0	759	3	US-09-303-518D-301	Sequence 301, App
35	14.4	90.0	789	3	US-09-902-540-8579	Sequence 8579, Ap
36	14.4	90.0	798	3	US-09-902-540-6036	Sequence 6036, Ap
37	14.4	90.0	816	3	US-09-902-540-7071	Sequence 7071, Ap
38	14.4	90.0	837	3	US-09-252-991A-4360	Sequence 4360, Ap
39	14.4	90.0	981	3	US-09-252-991A-15875	Sequence 15875, A
C 40	14.4	90.0	1032	3	US-09-252-991A-7887	Sequence 7887, Ap
C 41	14.4	90.0	1542	3	US-09-902-540-240	Sequence 240, App
42	14.4	90.0	1785	3	US-09-252-991A-4278	Sequence 4278, Ap
43	14.4	90.0	1899	3	US-09-902-540-3847	Sequence 3847, Ap
44	14.4	90.0	2219	2	US-08-606-322-1	Sequence 1, Appli
45	14.4	90.0	2289	3	US-09-489-039A-2837	Sequence 2837, Ap

ALIGNMENTS

RESULT 1
US-09-052-469-15
; Sequence 15, Application US/09052469
; Patent No. 6380360
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE.1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,469
; FILING DATE: Concurrently herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,582
; FILING DATE: 14-April-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/74165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 15:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /function= "N2765 primer"
US-09-052-469-15

Query Match 100.0%; Score 16; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Db 5 CGGCGGGCGGCATCGT 20

RESULT 2
US-08-422-582-15
; Sequence 15, Application US/08422582
; Patent No. 6485960
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 75 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,582
; FILING DATE: 14-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/53313 (MRC-006xxx)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..30
; OTHER INFORMATION: /function= "N2765 primer"
US-08-422-582-15

Query Match 100.0%; Score 16; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Db 5 CGGCGGGCGGCATCGT 20

RESULT 3
US-09-052-262-15
; Sequence 15, Application US/09052262
; Patent No. 6656681
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,262
; FILING DATE: Concurrently herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,582
; FILING DATE: 14-April-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/74118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /function= "N2765 primer"
US-09-052-262-15

Query Match      100.0%; Score 16; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
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Db 5 CGGCGGGCGGCATCGT 20

RESULT 4
US-09-902-540-2359
; Sequence 2359, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2359
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2359

Query Match      100.0%; Score 16; DB 3; Length 1281;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
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Db 257 CGGCGGGCGGCATCGT 272

RESULT 5
US-09-799-451-341/c
; Sequence 341, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Dimanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
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; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 341
; LENGTH: 13941
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1547)..(13120)
US-09-799-451-341

Query Match      100.0%; Score 16; DB 3; Length 13941;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
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Db 224 CGGCGGGCGGCATCGT 209

RESULT 6
US-08-658-136-4/c
; Sequence 4, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..13040
US-08-658-136-4

Query Match      100.0%; Score 16; DB 3; Length 14060;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGCGGGCGGCATCGT 16
Db 147 CGCGGGCGGCATCGT 132

RESULT 7
 US-10-083-246A-1/c
 ; Sequence 1, Application US/10083246A
 ; Patent No. 6916619
 ; GENERAL INFORMATION:
 ; APPLICANT: Athena Diagnostics
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC ANALYSIS OF POLYCYSTIC KIDNE
 ; TITLE OF INVENTION: DISEASE
 ; FILE REFERENCE: 1133/2002
 ; CURRENT APPLICATION NUMBER: US/10/083,246A
 ; CURRENT FILING DATE: 2002-10-15
 ; NUMBER OF SEQ ID NOS: 168
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 14136
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-083-246A-1

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Query Match      100.0%; Score 16; DB 3; Length 14136;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGCGGGCGGCATCGT 16
Db 224 CGCGGGCGGCATCGT 209

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RESULT 8
US-09-052-469-7/c
; Sequence 7, Application US/09052469
; Patent No. 6380360
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,469
; FILING DATE: Concurrently herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,582
; FILING DATE: 14-April-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:

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; NAME/KEY: misc_feature
; LOCATION: 11216..11276
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11894..11954
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
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; LOCATION: 12293..12353
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Possible hinge sequence"
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; NAME/KEY: misc_feature
; LOCATION: 279
; OTHER INFORMATION: /note= "Cleavage site"
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; US-09-052-469-7
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Query Match 100.0%; Score 16; DB 3; Length 14148;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||||
Db 224 CGGCGGGCGGCATCGT 209
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RESULT 9

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US-08-422-582-7/c
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; Patent No. 6485960
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 75 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,582
; FILING DATE: 14-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326470.3
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; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/53313 (MRC-006xx)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14148 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 212..13117
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 212..278
; OTHER INFORMATION: /note= "Probable signal sequence"
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; NAME/KEY: misc_feature
; LOCATION: 359..4574
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: sites at the following positions: 359, 476, 557, 572,
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "N-linked glycosylation
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; LOCATION: 8363..11741
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: sites at following locations: 8471, 8663, 8732, 8843,
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7949..8009
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 8288..8348
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 9434..9494
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10052..10112
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10178..10238
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Predicted transmembrane
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OTHER INFORMATION: domain"
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OTHER INFORMATION: /note= "Predicted transmembrane"
OTHER INFORMATION: domain"
FEATURE:
NAME/KEY: misc feature
LOCATION: 11894..11954
OTHER INFORMATION: /note= "Predicted transmembrane"
OTHER INFORMATION: domain"
FEATURE:
NAME/KEY: misc feature
LOCATION: 12293..12353
OTHER INFORMATION: /note= "Predicted transmembrane"
OTHER INFORMATION: domain"
FEATURE:
NAME/KEY: misc feature
LOCATION: 12377..12437
OTHER INFORMATION: /note= "Predicted transmembrane"
OTHER INFORMATION: domain"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 212..278
OTHER INFORMATION: /note= "Possible hinge sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 279
OTHER INFORMATION: /note= "Cleavage site"
US-09-052-262-7
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Query Match 100.0%; Score 16; DB 3; Length 14148;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CGCGGGCGGCATCGT 16
|||||
Db 224 CGCGGGCGGCATCGT 209
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RESULT 11
US-09-902-540-1100/c
; Sequence 1100, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1100
; LENGTH: 15447
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1100

Query Match 100.0%; Score 16; DB 3; Length 15447;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGGCGGCATCGT 16
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```
Db 3663 CGCGGGCGGCATCGT 3648

RESULT 12
US-08-323-443B-1
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/0A462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match 100.0%; Score 16; DB 2; Length 31571;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGGCGGCATCGT 16
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Db 3273 CGCGGGCGGCATCGT 3288

RESULT 13
US-08-658-136-2/c
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM
```

```

; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-2

Query Match 100.0%; Score 16; DB 3; Length 53526;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGGGGCGGCATCGT 16
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Db 3660 CGCGGGGGCGGCATCGT 3645

RESULT 14
US-08-658-136-1/c
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136

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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-1

Query Match 100.0%; Score 16; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGGGGCGGCATCGT 16
   |||||
Db 3660 CGCGGGGGCGGCATCGT 3645

RESULT 15
US-08-460-215A-1/c
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,215A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUGAN, DEBORAH
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-17.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-460-215A-1

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Query Match 100.0%; Score 16; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGGCATCGT 16
| | | | | | | | | | | | | | | |
Db 3660 CGGCGGGCGGCATCGT 3645

Search completed: May 9, 2006, 05:56:08
Job time : 45.0889 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: May 9, 2006, 05:26:49 ; Search time 387.378 Seconds
(without alignments)
341.553 Million cell updates/sec
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Perfect score: 16
Sequence: 1 cggcgggcggcgcgt 16
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	16	3	US-09-904-968A-20
C 2	16	100.0	485	5	Sequence 20, Appl
C 3	16	100.0	485	6	Sequence 292667,
4	16	100.0	619	7	Sequence 292667,
5	16	100.0	4062	6	Sequence 4510, Ap
C 6	16	100.0	12992	6	Sequence 875, App
C 7	16	100.0	13941	7	Sequence 89, Appl
C 8	16	100.0	14136	3	Sequence 341, App
C 9	16	100.0	14136	6	Sequence 244, App
C 10	16	100.0	14136	9	Sequence 1, Appli
C 11	16	100.0	14136	9	Sequence 5547, Ap
C 12	16	100.0	14136	9	Sequence 1, Appli
C 13	16	100.0	14169	9	Sequence 385, App
C 14	16	100.0	53522	3	Sequence 17056, A
15	16	100.0	9025608	6	Sequence 1, Appli
16	15	93.8	25	8	Sequence 515844,
17	15	93.8	261	8	Sequence 80381, A
C 18	15	93.8	486	7	Sequence 45611, A
C 19	15	93.8	511	6	Sequence 25, Appl
C 20	15	93.8	511	10	Sequence 25, Appl
21	15	93.8	540	7	Sequence 33759, A
22	15	93.8	615	7	Sequence 36162, A
23	15	93.8	687	7	Sequence 34646, A

24	15	93.8	738	8	US-10-425-115-34043	Sequence 34043, A
C 25	15	93.8	793	7	US-10-425-114-27555	Sequence 27555, A
26	15	93.8	819	6	US-10-369-493-32278	Sequence 32278, A
C 27	15	93.8	822	8	US-10-425-115-136862	Sequence 136862,
28	15	93.8	897	6	US-10-369-493-28520	Sequence 28520, A
29	15	93.8	897	6	US-10-369-493-31279	Sequence 31279, A
30	15	93.8	905	8	US-10-425-115-148261	Sequence 148261,
31	15	93.8	1020	9	US-10-494-495-2	Sequence 2, Appli
32	15	93.8	1032	6	US-10-156-761-3524	Sequence 3524, Ap
33	15	93.8	1269	6	US-10-369-493-31563	Sequence 31563, A
34	15	93.8	1355	7	US-10-767-701-13547	Sequence 13547, A
35	15	93.8	1389	7	US-10-425-114-4125	Sequence 4125, Ap
C 36	15	93.8	1448	7	US-10-425-114-23975	Sequence 23975, A
37	15	93.8	1704	7	US-10-282-122A-13582	Sequence 13582, A
38	15	93.8	1704	7	US-10-282-122A-14054	Sequence 14054, A
C 39	15	93.8	1721	8	US-10-425-115-55704	Sequence 55704, A
C 40	15	93.8	1875	7	US-10-437-963-36156	Sequence 36156, A
C 41	15	93.8	4786	7	US-10-437-963-18794	Sequence 18794, A
42	15	93.8	29870	9	US-10-494-495-1	Sequence 1, Appli
43	15	93.8	102634	9	US-10-915-740A-12	Sequence 12, Appl
C 44	15	93.8	135638	6	US-10-314-657-1	Sequence 1, Appli
C 45	15	93.8	135638	9	US-10-473-193-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-904-968A-20
; Sequence 20, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHADDEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 20
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer 1R1
US-09-904-968A-20
Query Match 100.0%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCGGGCGGCATCGT 16
| | | | | | | | | | | | | | | |
Db 1 CGCGGGCGGCATCGT 16
RESULT 2
US-10-027-632-292667/c
; Sequence 292667, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632

;
;
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292667
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-292667

Query Match 100.0%; Score 16; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGGCATCGT 16
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Db 20 CGGCGGGCGGCATCGT 5

RESULT 3
US-10-027-632-292667/c
; Sequence 292667, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292667
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-292667

Query Match 100.0%; Score 16; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGGCATCGT 16
|||
Db 20 CGGCGGGCGGCATCGT 5

RESULT 4
US-10-767-701-4510
; Sequence 4510, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4510
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS81577_1
US-10-767-701-4510

Query Match 100.0%; Score 16; DB 7; Length 619;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGGCATCGT 16
|||
Db 253 CGGCGGGCGGCATCGT 268

RESULT 5
US-10-156-761-875
; Sequence 875, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 875
; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4062)
US-10-156-761-875

Query Match 100.0%; Score 16; DB 6; Length 4062;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGGCGGCATCGT 16
|||
Db 2966 CGGCGGGCGGCATCGT 2981

RESULT 6
US-10-080-334-89/c

; Sequence 89, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/276,677
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 12992
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-080-334-89

Query Match 100.0%; Score 16; DB 6; Length 12992;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGGCGGCATCGT 16
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Db 65 CGCGGGCGGCATCGT 50

RESULT 7
US-10-302-172-341/c
; Sequence 341, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids a
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803_1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 341
; LENGTH: 13941
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1547)..(13120)
US-10-302-172-341

Query Match 100.0%; Score 16; DB 7; Length 13941;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGGCGGCATCGT 16
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Db 224 CGCGGGCGGCATCGT 209

RESULT 8
US-09-964-824A-244/c
; Sequence 244, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
; LENGTH: 14136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-244

Query Match 100.0%; Score 16; DB 3; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Best Local Similarity 100.0%; Score 16; DB 6; Length 14136;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 224 CGGCGGGCGGCATCGT 209

RESULT 9
US-10-083-246A-1/c
; Sequence 1, Application US/10083246A
; Publication No. US20030152936A1
; GENERAL INFORMATION:
; APPLICANT: Athena Diagnostics
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC ANALYSIS OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: 1133/2002
; CURRENT APPLICATION NUMBER: US/10/083,246A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 14136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-083-246A-1

Query Match 100.0%; Score 16; DB 6; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Best Local Similarity 100.0%; Score 16; DB 6; Length 14136;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 224 CGGCGGGCGGCATCGT 209

RESULT 10
US-10-843-641A-5547/c
; Sequence 5547, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5547
; LENGTH: 14136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5547

Query Match 100.0%; Score 16; DB 9; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Best Local Similarity 100.0%; Score 16; DB 9; Length 14136;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 224 CGGCGGGCGGCATCGT 209

RESULT 11
US-10-411-915-1/c
; Sequence 1, Application US/10411915
; Publication No. US20050100898A1
; GENERAL INFORMATION:
; APPLICANT: Athena Diagnostics
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC ANALYSIS OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: 1133/2005
; CURRENT APPLICATION NUMBER: US/10/411,915
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 10/083,246
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US 60/328,739
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 14136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-915-1

Query Match 100.0%; Score 16; DB 9; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Best Local Similarity 100.0%; Score 16; DB 9; Length 14136;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 224 CGGCGGGCGGCATCGT 209

RESULT 12
US-10-956-157-385/c
; Sequence 385, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 385
; LENGTH: 14136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-385

Query Match 100.0%; Score 16; DB 9; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Best Local Similarity 100.0%; Score 16; DB 9; Length 14136;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 224 CGGCGGGCGGCATCGT 209

RESULT 13
US-10-450-763-17056/c

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; Sequence 17056, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 17056
; LENGTH: 14169
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (212)..(9934)
; OTHER INFORMATION: 99% homologous to Homo sapiens Polycystic kidney disease 1
; OTHER INFORMATION: (PKD1) polypeptide,accession number W00870,Smith-Waterman Score=
; OTHER INFORMATION: 16983.
US-10-450-763-17056

Query Match      100.0%; Score 16; DB 9; Length 14169;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||||
Db      224 CGGCGGGCGGCATCGT 209

RESULT 14
US-09-904-968A-1/c
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHADDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 53522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-968A-1

Query Match      100.0%; Score 16; DB 3; Length 53522;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGGCGGGCGGCATCGT 16
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Db      3660 CGGCGGGCGGCATCGT 3645

RESULT 15
US-10-156-761-1
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; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      100.0%; Score 16; DB 6; Length 9025608;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGGCGGGCGGCATCGT 16
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Db      1064086 CGGCGGGCGGCATCGT 1064101

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OM nucleic - nucleic search, using sw model

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19: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	16	100.0	977	12	US-10-301-480-570506 Sequence 570506,
C 2	16	100.0	977	12	US-10-301-480-1183915 Sequence 1183915,
C 3	15	93.8	1424	18	US-11-096-568A-10796 Sequence 10796, A
C 4	15	93.8	1737	10	US-10-858-730-174 Sequence 174, Appl
C 5	15	93.8	14055	13	US-10-496-351-1 Sequence 1, Appl1
C 6	15	93.8	82746	13	US-10-496-351-56 Sequence 56, Appl
C 7	14.4	90.0	348	10	US-10-432-483-2 Sequence 2, Appl1
C 8	14.4	90.0	669	10	US-10-467-657-3407 Sequence 3407, Ap
C 9	14.4	90.0	687	10	US-10-467-657-5755 Sequence 5755, Ap
C 10	14.4	90.0	783	10	US-10-467-657-4281 Sequence 4281, Ap
C 11	14.4	90.0	852	10	US-10-467-657-2873 Sequence 2873, Ap
C 12	14.4	90.0	882	10	US-10-467-657-2875 Sequence 2875, Ap
C 13	14.4	90.0	991	10	US-10-750-185-63870 Sequence 63870, A
C 14	14.4	90.0	991	10	US-10-750-623-63870 Sequence 63870, A

15	14.4	90.0	1899	10	US-10-467-657-3439	Sequence 3439, Ap
16	14.4	90.0	1899	10	US-10-467-657-4631	Sequence 4631, Ap
C 17	14.4	90.0	2221	18	US-11-232-440-36	Sequence 36, Appl
18	14.4	90.0	8651	10	US-10-432-483-48	Sequence 48, Appl
C 19	14.4	90.0	1694969	13	US-10-506-454-1690	Sequence 1690, Ap
20	14	87.5	1593	18	US-11-079-463-4797	Sequence 4797, Ap
21	14	87.5	1930	18	US-11-144-947-172	Sequence 172, App
C 22	14	87.5	2442	13	US-10-469-469-276	Sequence 276, App
23	14	87.5	2683	18	US-11-144-947-301	Sequence 301, App
24	13.4	83.8	24	10	US-10-310-914A-169492	Sequence 169492,
25	13.4	83.8	255	10	US-10-909-125-1990	Sequence 1990, Ap
26	13.4	83.8	389	7	US-09-925-065A-502219	Sequence 502219,
27	13.4	83.8	396	18	US-11-250-759-167	Sequence 167, App
28	13.4	83.8	434	7	US-09-925-065A-480598	Sequence 480598,
29	13.4	83.8	434	7	US-09-925-065A-480599	Sequence 480599,
C 30	13.4	83.8	435	10	US-10-467-657-709	Sequence 709, App
31	13.4	83.8	447	10	US-10-467-657-711	Sequence 711, App
32	13.4	83.8	471	7	US-09-925-065A-386550	Sequence 386550,
33	13.4	83.8	471	7	US-09-925-065A-386551	Sequence 386551,
34	13.4	83.8	471	7	US-09-925-065A-386552	Sequence 386552,
35	13.4	83.8	476	12	US-10-301-480-455124	Sequence 455124,
36	13.4	83.8	476	12	US-10-301-480-455125	Sequence 455125,
37	13.4	83.8	476	12	US-10-301-480-455126	Sequence 455126,
38	13.4	83.8	476	12	US-10-301-480-1068533	Sequence 1068533,
39	13.4	83.8	476	12	US-10-301-480-1068534	Sequence 1068534,
40	13.4	83.8	476	12	US-10-301-480-1068535	Sequence 1068535,
C 41	13.4	83.8	512	17	US-11-181-587-21	Sequence 21, Appl
C 42	13.4	83.8	651	17	US-11-143-401-13	Sequence 13, Appl
C 43	13.4	83.8	654	17	US-11-052-554A-710	Sequence 710, App
44	13.4	83.8	680	12	US-10-301-480-536297	Sequence 536297,
45	13.4	83.8	680	12	US-10-301-480-1149706	Sequence 1149706,

ALIGNMENTS

RESULT 1
US-10-301-480-570506/c
; Sequence 570506, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 570506
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-570506

Query Match 100.0%; Score 16; DB 12; Length 977;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGGCGGCATCGT 16
| | | | | | | | | | | | | | | |
Db 339 CGCGGGCGGCATCGT 324

RESULT 2
US-10-301-480-1183915/c
; Sequence 1183915, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1183915
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-1183915

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Query Match      100.0%; Score 16; DB 12; Length 977;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CGCGGGCGGCATCGT 16
Db 339 CGCGGGCGGCATCGT 324

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RESULT 3
US-11-096-568A-10796
; Sequence 10796, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10796
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1424)
; OTHER INFORMATION: Ceres Seq. ID no. 13597194
US-11-096-568A-10796

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Query Match          93.8%; Score 15; DB 18; Length 1424;
Best Local Similarity 100.0%; Pred. NO. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CGCGGGCGGCATCG 15
Db 240 CGCGGGCGGCATCG 254

RESULT 4
US-10-858-730-174/c
; Sequence 174, Application US/10858730
; Publication No. US2005025568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
; US-10-858-730-174

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Query Match      93.8%; Score 15; DB 10; Length 1737;
Best Local Similarity 100.0%; Pred. NO. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CGCGGGCGGCATCG 15
Db 991 CGCGGGCGGCATCG 977

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RESULT 5
US-10-496-351-1/c
; Sequence 1, Application US/10496351
; Publication No. US20060084141A1
; GENERAL INFORMATION:
; APPLICANT: Floss, Heinz
; APPLICANT: Yu, Tin-Wein
; APPLICANT: Leistner, Eckard
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Maytansinoid Antitumor Agent
; FILE REFERENCE: UWASH-06712
; CURRENT APPLICATION NUMBER: US/10/496,351
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 14055
; TYPE: DNA
; ORGANISM: Actinosynnema pretiosum
US-10-496-351-1

```

Query Match 93.8%; Score 15; DB 13; Length 14055;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0

Qy 1 CGCGGGCGGCATCG 15
|||
db 13723 CGCGGGCGGCATCG 13709

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RESULT 6
US-10-496-351-56
; Sequence 56, Application US/10496351
; Publication NO. US20060084141A1
; GENERAL INFORMATION:
; APPLICANT: Floss, Heinz
; APPLICANT: Yu, Tin-Wein
; APPLICANT: Leistner, Eckard
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Maytansinoid Antitumor Agent
; TITLE OF INVENTION: Ansamitocin
; FILE REFERENCE: UWASH-06712
; CURRENT APPLICATION NUMBER: US/10/496,351
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 82746

```



```

; TYPE: DNA
; ORGANISM: Actinosynnema pretiosum
US-10-496-351-56

Query Match          93.8%; Score 15; DB 13; Length 82746;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGCGGGCGGCATCG 15
Db      23319 CGGCGGGCGGCATCG 23333

RESULT 7
US-10-432-483-2
; Sequence 2, Application US/10432483
; Publication No. US20050260699A1
; GENERAL INFORMATION:
; APPLICANT: deSouza, Mervyn L.
; APPLICANT: Jessen, Holly
; APPLICANT: Schroeder, William A.
; APPLICANT: Gokarn, Ravi R.
; TITLE OF INVENTION: CAROTENOID BIOSYNTHESIS
; FILE REFERENCE: 12799-002US1
; CURRENT APPLICATION NUMBER: US/10/432,483
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PCT/US01/43906
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,749
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Agromyces mediolanus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(345)
US-10-432-483-2

Query Match          90.0%; Score 14.4; DB 10; Length 348;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGCGGGCGGCATCGT 16
Db      107 CGGCGGGCGGCCTCGT 122

RESULT 8
US-10-467-657-3407/c
; Sequence 3407, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3407
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3407
```

```

Query Match          90.0%; Score 14.4; DB 10; Length 669;
Best Local Similarity 93.8%; Pred. No. 99;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGCGGGCGGCATCGT 16
Db      104 CGGCGGACGGCATCGT 89

RESULT 9
US-10-467-657-5755/c
; Sequence 5755, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5755
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5755

Query Match          90.0%; Score 14.4; DB 10; Length 687;
Best Local Similarity 93.8%; Pred. No. 99;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGCGGGCGGCATCGT 16
Db      338 CAGCGGGCGGCATCGT 323

RESULT 10
US-10-467-657-4281
; Sequence 4281, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4281
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4281

Query Match          90.0%; Score 14.4; DB 10; Length 783;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGGCGGGCGGCATCGT 16
Db      104 CGGCGGACGGCATCGT 89
```

Db 566 CGGCGGACGGCATCGT 581

RESULT 11

US-10-467-657-2873
; Sequence 2873, Application US/10467657
; Publication No. US20050260581A1

GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2873
; LENGTH: 852
; TYPE: DNA

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-2873

Query Match 90.0%; Score 14.4; DB 10; Length 852;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
||||| |||||||
Db 744 CGGCGGGCAGCATCGT 759

RESULT 12

US-10-467-657-2875/c
; Sequence 2875, Application US/10467657
; Publication No. US20050260581A1

GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2875
; LENGTH: 882
; TYPE: DNA

; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-2875

Query Match 90.0%; Score 14.4; DB 10; Length 882;
Best Local Similarity 93.8%; Pred. No. 93;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
||||| |||||||
Db 121 CGGCGGGCAGCATCGT 106

RESULT 13

US-10-750-185-63870/c
; Sequence 63870, Application US/10750185
; Publication No. US20050260603A1

; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 63870
; LENGTH: 991
; TYPE: DNA
; ORGANISM: Bovine 19866881191767
US-10-750-185-63870

Query Match 90.0%; Score 14.4; DB 10; Length 991;
Best Local Similarity 93.8%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
||||| ||||||| ||||
Db 450 CGGACGGCGGCATCGT 435

RESULT 14

US-10-750-623-63870/c
; Sequence 63870, Application US/10750623
; Publication No. US20050287531A1

GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 63870
; LENGTH: 991
; TYPE: DNA
; ORGANISM: Bovine 19866881191767
US-10-750-623-63870

Query Match 90.0%; Score 14.4; DB 10; Length 991;
Best Local Similarity 93.8%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
||||| ||||||| ||||
Db 450 CGGACGGCGGCATCGT 435

RESULT 15

US-10-467-657-3439
; Sequence 3439, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3439
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3439

Query Match 90.0%; Score 14.4; DB 10; Length 1899;
Best Local Similarity 93.8%; Pred. No. 78;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
||||| |||||||
Db 656 CGGCGGACGGCATCGT 671

Search completed: May 9, 2006, 06:39:10
Job time : 361.956 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:50:29 ; Search time 0.001 Seconds
(without alignments)
2.912 Million cell updates/sec

Title: US-09-904-968A-4-COPY
Perfect score: 26
Sequence: 1 ccacctcgcgccttcctaagcat 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 5 seqs, 56 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5 summaries

Database : estdb4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11.4	43.8	15	1	BQ595631	ACCESSION:BQ595631
C 2	7.8	30.0	11	1	BQ111753	ACCESSION:BQ111753
C 3	7	26.9	10	1	AJ734312	ACCESSION:AJ734312
4	7	26.9	10	1	CA795700	ACCESSION:CA795700
5	7	26.9	10	1	AJ591555	ACCESSION:AJ591555

ALIGNMENTS

RESULT 1
BQ595631
LOCUS
DEFINITION
E012693-024-022-B04-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
CDNA clone 024-022-B04 5-PRIME, mRNA sequence.
ACCESSION
BQ595631
VERSION
BQ595631.1 GI:26125214
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 22 row: B column: 04
Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES
Location/Qualifiers
1..15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="taxon:161934"
/clone="024-022-B04"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 43.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.24;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CATCGCCCTTCC 19
||||| |||||

Db 3 CATCGTCCCTTCC 15

RESULT 2

BQ111753/c

LOCUS

DEFINITION

EST597329 mixed potato tissues Solanum tuberosum cDNA clone STMCC84

5' end, mRNA sequence.

ACCESSION

BQ111753

VERSION

BQ111753.1 GI:20163715

KEYWORDS

EST.

SOURCE

ORGANISM

Solanum tuberosum (potato)

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum.

REFERENCE

1 (bases 1 to 11)

AUTHORS

Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamycheva,S.A.

TITLE

Generation of a set of potato cDNA clones for microarray analyses

JOURNAL

Unpublished (2002)

COMMENT

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics

Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/
Seq primer: T3.

FEATURES

source

1..11

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec or Binjte"

/db_xref="taxon:4113"

/clone="STMCC84"

http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES

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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="587C11"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
misc_feature 1. .10
/note="T-DNA flanking sequence
left border"

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTC 7
|||||
Db 4 CCACCTC 10

Search completed: May 9, 2006, 16:50:29
Job time : 0.001 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:58:22 ; Search time 0.001 Seconds
(without alignments)
163.436 Million cell updates/sec

Title: US-09-904-968A-4-COPY
Perfect score: 26
Sequence: 1 ccacctcctgcctcccttcctaagcat 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 283 seqs, 3143 residues

Total number of hits satisfying chosen parameters: 566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 284 summaries

Database : gedb4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	26	1	AX440500
2	12.8	49.2	18	1	AR492979
3	12.2	46.9	17	1	CQ615502
4	12.2	46.9	17	1	CQ622815
5	12.2	46.9	17	1	AR456565
6	12.2	46.9	17	1	AR463878
7	12.2	46.9	17	1	AX217105
8	10.8	41.5	15	1	CS005007
9	10.8	41.5	15	1	CS005022
10	10.8	41.5	15	1	CS005061
11	10.8	41.5	15	1	CS005071
12	10.8	41.5	15	1	CS005079
13	10.8	41.5	15	1	I61479
14	10.8	41.5	15	1	I61572
15	10.8	41.5	15	1	I61599
16	10.8	41.5	15	1	I61604
17	10.8	41.5	15	1	I61608
18	10.8	41.5	15	1	AX635896
19	10.8	41.5	15	1	AX635911
20	10.8	41.5	15	1	AX635950
21	10.8	41.5	15	1	AX635960
22	10.8	41.5	15	1	AX635968
23	9.8	37.7	13	1	A89148
24	9.8	37.7	13	1	BD066661
25	9.8	37.7	13	1	AR637821
26	9.4	36.2	11	1	AX627110
27	9.4	36.2	11	1	AX627937
28	9.4	36.2	11	1	AX629196
29	9.4	36.2	13	1	A89149
30	9.4	36.2	13	1	BD066662
31	9.4	36.2	13	1	BD091501
32	9.4	36.2	13	1	I04667
33	9	34.6	10	1	AR016487

C 34	9	34.6	10	1	AR078332
C 35	9	34.6	10	1	AR173052
C 36	9	34.6	10	1	BD105402
37	9	34.6	10	1	BD240558
38	9	34.6	11	1	CQ837376
39	9	34.6	11	1	CQ837875
40	9	34.6	11	1	AX471300
41	9	34.6	11	1	AX623401
42	9	34.6	11	1	AX623781
C 43	9	34.6	11	1	AX624932
44	9	34.6	11	1	AX628454
45	9	34.6	11	1	AX630822
46	9	34.6	11	1	AX631202
C 47	9	34.6	11	1	AX632353
48	8.8	33.8	12	1	A71544
49	8.8	33.8	12	1	AR024081
50	8.8	33.8	12	1	AR030073
C 51	8.8	33.8	12	1	BD270711
52	8.8	33.8	12	1	AR224300
C 53	8.8	33.8	12	1	AX010703
54	8.8	33.8	12	1	AX711075
55	8.8	33.8	12	1	BD001185
56	8.8	33.8	12	1	BD001614
C 57	8.4	32.3	10	1	AR030034
58	8.4	32.3	10	1	AR043160
59	8.4	32.3	10	1	AR074660
C 60	8.4	32.3	10	1	BD238681
61	8.4	32.3	10	1	BD239457
C 62	8.4	32.3	10	1	BD239777
63	8.4	32.3	10	1	BD240380
64	8.4	32.3	10	1	CS052685
65	8.4	32.3	10	1	E27859
66	8.4	32.3	10	1	I22209
C 67	8.4	32.3	10	1	AX152425
C 68	8.4	32.3	10	1	AX152861
69	8.4	32.3	10	1	AX152959
70	8.4	32.3	10	1	AX152960
C 71	8.4	32.3	10	1	AX153190
C 72	8.4	32.3	10	1	AX302593
C 73	8.4	32.3	10	1	BD007795
74	8.4	32.3	11	1	AR029871
75	8.4	32.3	11	1	CQ832679
C 76	8.4	32.3	11	1	CQ832959
C 77	8.4	32.3	11	1	CQ833029
78	8.4	32.3	11	1	CQ835576
79	8.4	32.3	11	1	CQ836387
C 80	8.4	32.3	11	1	CQ836706
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101	8.4	32.3	11	1	AX628882
C 102	8.4	32.3	11	1	AX629566
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C 104	8.4	32.3	11	1	AX629791
C 105	8.4	32.3	11	1	AX630124
C 106	8.4	32.3	11	1	AX630572

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C 127	8	30.8	10	1	AR575231	ACCESSION:AR575231
C 128	8	30.8	10	1	AX467563	ACCESSION:AX467563
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C 165	7.8	30.0	11	1	Q0833593	ACCESSION:Q0833593
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C 168	7.8	30.0	11	1	Q0837760	ACCESSION:Q0837760
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C 199	7.8	30.0	11	1	AX630373	ACCESSION:AX630373
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C 258 7.4 28.5 10 1 AR351721 ACCESSION:AR351721
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261 7.4 28.5 10 1 AX033052 ACCESSION:AX033052
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C 282 7.4 28.5 10 1 AX753477 ACCESSION:AX753477
C 283 7.4 28.5 10 1 BD007796 ACCESSION:BD007796
C 284 7.4 28.5 10 1 BD007887 ACCESSION:BD007887

ALIGNMENTS

RESULT 1
AX440500
LOCUS AX440500 26 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 4 from Patent WO0206529.
ACCESSION AX440500
VERSION AX440500.1 GI:21665303
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Germino,G.G., Watnick,T.J. and Phakdeekitcharoen,B.
TITLE Detection and treatment of polycystic kidney disease
JOURNAL Patent: WO 0206529-A 4 24-JAN-2002;
The Johns Hopkins University School of Medicine (US)
FEATURES
source
1. .26
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="PCR primer BPR9"

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Best Local Similarity 100.0%; Pred. No. 0.042;
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QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26
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Db 1 CCACCTCATCGCCCTTCCTAAGCAT 26

RESULT 2
AR492979
LOCUS AR492979 18 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 11 from patent US 6720137.
ACCESSION AR492979

VERSION AR492979.1 GI:47264283
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Roder,M., Plaschke,J. and Ganai,M.
TITLE Microsatellite markers for plants of the species Triticum aestivum and Tribe triticeae and the use of said markers
JOURNAL Patent: US 6720137-A 11 13-APR-2004;
Institut fur Pflanzengenetik und Kulturpflanzenforschung;
Gatersleben;
DEX;
FEATURES
source
Location/Qualifiers
1. .18
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Db 2 CGACCTGATCGCCCT 17

RESULT 3
CQ615502
LOCUS CQ615502 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 242 from Patent WO0192524.
ACCESSION CQ615502
VERSION CQ615502.1 GI:41665720
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 242 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
1. .17
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 CATCCTCGCCCTCCT 17

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DEFINITION Sequence 7555 from Patent WO0192524.
ACCESSION CQ622815
VERSION CQ622815.1 GI:41673033
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
TITLE
JOURNAL
Patent: US 6720137-A 11 13-APR-2004;
Institut fur Pflanzengenetik und Kulturpflanzenforschung;
Gatersleben;
DEX;
FEATURES
source
Location/Qualifiers
1. .18
/organism="unknown"
/mol_type="genomic DNA"

AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7555 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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AR456565
LOCUS AR456565 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 242 from patent US 6686188.
ACCESSION AR456565
VERSION AR456565.1 GI:42691622
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 242 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES Location/Qualifiers
source 1. .17
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Db 1 CATCCTCGCCCTTCCT 17
RESULT 6
AR463878/c
LOCUS AR463878 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7555 from patent US 6686188.
ACCESSION AR463878
VERSION AR463878.1 GI:42698935
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7555 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES Location/Qualifiers
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RESULT 7
AX217105/c
LOCUS AX217105 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2547 from Patent WO0159103.
ACCESSION AX217105
VERSION AX217105.1 GI:15527166
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2547 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1. .17
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Best Local Similarity 82.4%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 17 CTCATGGCCTCTTCATA 1
RESULT 8
CS005007
LOCUS CS005007 15 bp DNA linear PAT 07-FEB-2005
DEFINITION Sequence 3035 from Patent EP1502950.
ACCESSION CS005007
VERSION CS005007.1 GI:58740362
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified.
1
AUTHORS Stinchcomb,D.T., Chowrira,B., Direnzo,A., Draper,K.G., Dudycz,L.W., Grimm,S., Karpeisky,A., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method for purifying chemically modified RNA
JOURNAL Patent: EP 1502950-A 3035 02-FEB-2005;
Ribozyme Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1. .15
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Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 3035 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .15
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 GCCCCTTCCTAAGC 24
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Db 1 GTCCCTTCCTCAGC 14
RESULT 19
AX635911
LOCUS AX635911 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3050 from Patent EP1260586.
ACCESSION AX635911
VERSION AX635911.1 GI:28471525
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 3050 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .15
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCACCTCATCGCC 14
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Db 2 CCACCTCACC GCC 15
RESULT 20
AX635950
LOCUS AX635950 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3089 from Patent EP1260586.
ACCESSION AX635950
VERSION AX635950.1 GI:28471564
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,

Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 3089 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 GCCCCTTCCTAAGC 24
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTCCCTTCCTCAGC 14
RESULT 21
AX635960
LOCUS AX635960 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3099 from Patent EP1260586.
ACCESSION AX635960
VERSION AX635960.1 GI:28471574
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 3099 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 GCCCCTTCCTAAGC 24
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Db 2 GTCCCTTCCTCAGC 15
RESULT 22
AX635968
LOCUS AX635968 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3107 from Patent EP1260586.
ACCESSION AX635968
VERSION AX635968.1 GI:28471582
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes

genes
JOURNAL Patent: EP 1260586-A 3107 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1..15
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/mol_type="unassigned RNA"
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Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGCGCCCTTCCT 20
| | | | |
Db 2 CATGGTCCCTTCCT 15

RESULT 23
A89148
LOCUS A89148 13 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1296 from Patent WO9833904.
ACCESSION A89148
VERSION A89148.1 GI:6737718
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 13)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1296 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers
source 1..13
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/db_xref="taxon:32644"

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 46;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAAGC 24
| | | | |
Db 1 CTCCTTCCTAAGC 13

RESULT 24
BD066661
LOCUS BD066661 13 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066661
VERSION BD066661.1 GI:22612264
KEYWORDS JP 2001511000-A/1296.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 13)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1296 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1296
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..13

FT Location/Qualifiers
source 1..13
/organism='Unknown'.
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 46;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAAGC 24
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Db 1 CTCCTTCCTAAGC 13

RESULT 25
AR637821/c
LOCUS AR637821 13 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 35 from patent US 6855866.
ACCESSION AR637821
VERSION AR637821.1 GI:62771643
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Weterings,K., Apuya,N.R. and Goldberg,R.B.
TITLE Polynucleotides useful for modulating transcription
JOURNAL Patent: US 6855866-A 35 15-FEB-2005;
The Regents of the University of California; Oakland, CA
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="genomic DNA"

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 46;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAAGCAT 26
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Db 13 CCTTCATAAGCTT 1

RESULT 26
AX627110/c
LOCUS AX627110 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4151 from Patent WO02053774.
ACCESSION AX627110
VERSION AX627110.1 GI:28455148
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4151 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 36.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATCGCCCTTC 18

Db 11 ATGCCCTTC 1
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RESULT 27
AX627937
LOCUS
DEFINITION Sequence 4978 from Patent WO02053774. linear PAT 21-FEB-2003
ACCESSION AX627937
VERSION AX627937.1 GI:28455975
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4978 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
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Query Match 36.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CACCTCATCGC 12
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Db 1 CACCTCATCCC 11
RESULT 28
AX629196/c
LOCUS
DEFINITION Sequence 6237 from Patent WO02053774. linear PAT 21-FEB-2003
ACCESSION AX629196
VERSION AX629196.1 GI:28457234
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6237 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
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/db_xref="taxon:9606"
Query Match 36.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CTTCCTAAGCA 25
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Db 11 CTTCCTCAGCA 1
RESULT 29
A89149
LOCUS
DEFINITION Sequence 1297 from Patent WO9833904. linear PAT 22-JAN-2000
ACCESSION A89149

VERSION A89149.1 GI:6737719
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE
1 (bases 1 to 13)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1297 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1. .13
Location/Qualifiers
/organism="unidentified"
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/db_xref="taxon:32644"
Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 CCTTCCTAAGC 24
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Db 1 CCTCCTAAGC 11
RESULT 30
BD066662
LOCUS
DEFINITION An antisense oligonucleotide preparation method. linear PAT 27-AUG-2002
ACCESSION BD066662
VERSION BD066662.1 GI:22612265
KEYWORDS JP 2001511000-A/1297.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 13)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1297 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/1297
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
1. .13
source
/organism="Unknown".
Location/Qualifiers
1. .13
/organism="unidentified"
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Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 CCTTCCTAAGC 24
|||||
Db 1 CCTCCTAAGC 11
RESULT 31
BD091501
LOCUS
DEFINITION Transcriptional activator. linear PAT 27-AUG-2002
ACCESSION BD091501
VERSION BD091501.1 GI:22637112
KEYWORDS WO 0132860-A/2.

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 (bases 1 to 13)
TITLE Kataoka,K.
JOURNAL Transcriptional activator
COMMENT Patent: WO 0132860-A 2 10-MAY-2001;
OTSUKA PHARMACEUTICAL CO LTD,KOSUKE KATAOKA
OS Artificial Sequence
PN WO 0132860-A/2
PD 10-MAY-2001
PF 15-FEB-2000 WO 2000JP000841
PR 04-NOV-1999 JP 99P 314335
PI KOSUKE KATAOKA
PC C12N15/11,C01G11/00,C01G13/04,C01G7/00,C07C323/52,C07H23/00 CC
Maf recognition element
FH Key Location/Qualifiers.
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source
1. .13
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CTTCCCTAAGCA 25
||| |||||
Db 3 CTTACTAAGCA 13
RESULT 32
I04667
LOCUS I04667 13 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 13 from Patent EP 0200986.
ACCESSION I04667
VERSION I04667.1 GI:591573
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Gubler,U.A., Lomedico,P.T. and Mizel,S.B.
TITLE Recombinant human interleukin-1
JOURNAL Patent: EP 0200986-A1 13 12-NOV-1986;
FEATURES Location/Qualifiers
source
1. .13
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CTTCCCTAAGCA 25
||||| |||||
Db 1 CTTCCTGAGCA 11
RESULT 33
AR016487/c
LOCUS AR016487 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776744.
ACCESSION AR016487
VERSION AR016487.1 GI:3972764
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Glazer,P.M., Lin,L.Michael. and George,J.
TITLE Methods and compositions for effecting homologous recombination

JOURNAL Patent: US 5776744-A 2 07-JUL-1998;
FEATURES Location/Qualifiers
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
|||||
Db 9 CCCCTTCCT 1
RESULT 34
AR078332/c
LOCUS AR078332 10 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5962426.
ACCESSION AR078332
VERSION AR078332.1 GI:10005078
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Glazer,P.M.
TITLE Triple-helix forming oligonucleotides for targeted mutagenesis
JOURNAL Patent: US 5962426-A 1 05-OCT-1999;
FEATURES Location/Qualifiers
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
|||||
Db 9 CCCCTTCCT 1
RESULT 35
AR173052/c
LOCUS AR173052 10 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6303376.
ACCESSION AR173052
VERSION AR173052.1 GI:17912543
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Glazer,P.M.
TITLE Methods of targeted mutagenesis using triple-helix forming oligonucleotides
JOURNAL Patent: US 6303376-A 1 16-OCT-2001;
FEATURES Location/Qualifiers
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
|||||
Db 9 CCCCTTCCT 1
RESULT 36

BD105402/c
LOCUS BD105402 10 bp DNA linear PAT 27-AUG-2002
DEFINITION 5-Pyrimidine-containing nucleic acid, and reversible ligation method using the same.
ACCESSION BD105402
VERSION BD105402.1 GI:22650976
KEYWORDS JP 2001348398-A/2. synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Saito,I., Fujimoto,K., Matsuda,S. and Yoshino,H.
TITLE 5-Pyrimidine-containing nucleic acid, and reversible ligation method using the same
JOURNAL Patent: JP 2001348398-A 2 18-DEC-2001;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Artificial Sequence
PN JP 2001348398-A/2
PD 18-DEC-2001
PF 05-JAN-2001 JP 2001000750
PI ISAO SAITO,KENZO FUJIMOTO,SHIGEO MATSUDA,HIDEAKI YOSHINO PC C07H21/04,C07H1/00,C07H19/10,C12P19/30,C12Q1/68 CC Description of Artificial Sequence:template DNA;named ODN A3 FH Key
Location/Qualifiers
FT source 1..10
FT /organism='Artificial Sequence'.
FEATURES
source
1..10 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 TCCTAAGCA 25
Db 9 TCCTAAGCA 1
RESULT 37
BD240558
LOCUS BD240558 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240558
VERSION BD240558.1 GI:33050328
KEYWORDS JP 2002534056-A/1976.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1976 15-OCT-2002;
COMMENT GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1976
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR

19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..10 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTTCTAAG 23
Db 2 CTTCTAAG 10
RESULT 38
CQ837376
LOCUS CQ837376 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2434 from Patent WO2004059001.
ACCESSION CQ837376
VERSION CQ837376.1 GI:50836910
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2434 15-JUL-2004;
HENKEL KOMMANDITGESELLSCHAFT AUF AKTIEN (DE)
FEATURES
source
1..11 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
Db 3 CCCCTTCCT 11
RESULT 39
CQ837875
LOCUS CQ837875 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2933 from Patent WO2004059001.
ACCESSION CQ837875
VERSION CQ837875.1 GI:50837409
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE 1
AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
          Conradt,M. and Hofmann,K.
TITLE     Method for determining markers of human facial skin
JOURNAL   Patent: WO 2004059001-A 2933 15-JUL-2004;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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Query Match      34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
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Db 3 CCCCTTCCT 11

RESULT 40
AX471300
LOCUS      AX471300 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 877 from Patent WO02053773.
ACCESSION  AX471300
VERSION     AX471300.1 GI:22206425
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
TITLE     Method for determining skin stress or skin ageing in vitro
JOURNAL   Patent: WO 02053773-A 877 11-JUL-2002;
          HENKEL KGAA (DE)
FEATURES  Location/Qualifiers
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Query Match      34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
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Db 3 CCCCTTCCT 11

RESULT 41
AX623401
LOCUS      AX623401 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 442 from Patent WO02053774.
ACCESSION  AX623401
VERSION     AX623401.1 GI:28451342
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 442 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
    |||
Db 3 CCCCTTCCT 11

RESULT 42
AX623781
LOCUS      AX623781 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 822 from Patent WO02053774.
ACCESSION  AX623781
VERSION     AX623781.1 GI:28451722
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 822 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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Query Match      34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
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Db 3 CCCCTTCCT 11

RESULT 43
AX624932/c
LOCUS      AX624932 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1973 from Patent WO02053774.
ACCESSION  AX624932
VERSION     AX624932.1 GI:28452873
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 1973 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
          source
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Query Match      34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
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QY 12 CCCCTTCCT 20
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Db 3 CCCCTTCCT 11

RESULT 44
AX624932/c
LOCUS      AX624932 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1973 from Patent WO02053774.
ACCESSION  AX624932
VERSION     AX624932.1 GI:28452873
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 1973 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCAT 9
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Db 11 CCACCTCAT 3
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RESULT 44
AX628454
LOCUS AX628454 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5495 from Patent WO02053774.
ACCESSION AX628454
VERSION AX628454.1 GI:28456492
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5495 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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QY 12 CCCCTTCCT 20
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Db 3 CCCCTTCCT 11
Query Match 34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
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Db 3 CCCCTTCCT 11
RESULT 45
AX630822
LOCUS AX630822 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7863 from Patent WO02053774.
ACCESSION AX630822
VERSION AX630822.1 GI:28458862
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7863 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 56;
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QY 12 CCCCTTCCT 20
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Db 3 CCCCTTCCT 11
RESULT 46
AX631202
LOCUS AX631202 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8244 from Patent WO02053774.
ACCESSION AX631202

VERSION AX631202.1 GI:28459246
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8244 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
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Db 3 CCCCTTCCT 11
RESULT 47
AX632353/c
LOCUS AX632353 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9395 from Patent WO02053774.
ACCESSION AX632353
VERSION AX632353.1 GI:28467968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9395 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACCTCAT 9
|||||
Db 11 CCACCTCAT 3
RESULT 48
A71544
LOCUS A71544 12 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 103 from Patent WO9813521.
ACCESSION A71544
VERSION A71544.1 GI:4775156
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS (bases 1 to 12)
TITLE Fesce,R. and Consalez,G.
METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION

JOURNAL Patent: WO 9813521-A 103 02-APR-1998;
FESCE RICCARDO (IT)
FEATURES Location/Qualifiers
source 1. .12
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CACCTCATCGCC 13
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Db 1 CGCCTCATTGCC 12
RESULT 49
AR024081
LOCUS AR024081 12 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 31 from patent US 5795778.
ACCESSION AR024081
VERSION AR024081.1 GI:3977375
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 5795778-A 31 18-AUG-1998;
FEATURES Location/Qualifiers
source 1. .12
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/mol_type="unassigned DNA"
Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 CCTCATCGCCCC 15
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Db 1 CCTCCACGCCCC 12
RESULT 50
AR030073
LOCUS AR030073 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 262 from patent US 5861244.
ACCESSION AR030073
VERSION AR030073.1 GI:5943287
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 262 19-JAN-1999;
FEATURES Location/Qualifiers
source 1. .12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 CCTCATCGCCCC 15
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Db 1 CCTCTTCCCCC 12

RESULT 51
BD270711/c
LOCUS BD270711 12 bp DNA linear PAT 17-JUL-2003
DEFINITION Selection system.
ACCESSION BD270711
VERSION BD270711.1 GI:33080479
KEYWORDS JP 2002514413-A/38.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 12)
AUTHORS Riechmann,L., Kristensen,P., Jestin,J.L. and Winter,G.P.
TITLE Selection system
JOURNAL Patent: JP 2002514413-A 38 21-MAY-2002;
COMMENT DIVERSYS LTD
OS Artificial Sequence
PN JP 2002514413-A/38
PD 21-MAY-2002
PF 13-MAY-1999 JP 2000548446
PR 13-MAY-1998 GB 9810223.9,13-MAY-1998 GB 9810228.8 PI
LUTZ RIECHMANN,PETER KRISTENSEN,JEAN LUC JESTIN,GREGORY PAUL PI
WINTER
PC C12N15/00,C12N7/02,C12N15/00
CC Description of Artificial Sequence:PRIMER/POLYPEPTIDE FH Key
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FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .12
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCACCTCATCGC 12
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Db 12 CCACATCTTCGC 1
RESULT 52
AR224300
LOCUS AR224300 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 31 from patent US 6440719.
ACCESSION AR224300
VERSION AR224300.1 GI:23333077
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 6440719-A 31 27-AUG-2002;
FEATURES Ribozyme Pharmaceuticals, Inc.; Boulder, CO
source Location/Qualifiers
1. .12
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 CCTCATCGCCCC 15
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Db 1 CCTCCACGCCCC 12
RESULT 53
AX010703/c

LOCUS AX010703 12 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 45 from Patent WO9958655.
ACCESSION AX010703
VERSION AX010703.1 GI:9997496
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kristensen,P., Jestin,J.L., Winter,G.P. and Riechmann,L.
TITLE Selection system
JOURNAL Patent: WO 9958655-A 45 18-NOV-1999;
KRISTENSEN PETER (DK); JESTIN JEAN LUC (FR); MEDICAL RES COUNCIL
(GB); WINTER GREGORY PAUL (GB); RIECHMANN LUTZ (GB)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCACCTCATCGC 12
Db 12 CCACATCTTCGC 1
RESULT 54
AX711075
LOCUS AX711075 12 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 375 from Patent EP1288296.
ACCESSION AX711075
VERSION AX711075.1 GI:29787456
KEYWORDS
SOURCE Herpes simplex virus unknown type
ORGANISM Herpes simplex virus unknown type
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
REFERENCE 1
AUTHORS Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 375 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1..12
Location/Qualifiers
/organism="Herpes simplex virus unknown type"
/mol_type="unassigned RNA"
/db_xref="taxon:126283"
Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCTCATCGCCCC 15
Db 1 CCTCCACGCCCC 12
RESULT 55
BD001185
LOCUS BD001185 12 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001185
VERSION BD001185.1 GI:18625744
KEYWORDS JP 2000342285-A/345.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 12)

AUTHORS Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 345 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342285-A/345
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
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14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN,PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00,C12N9/22/(C12N5/10,C12R1:91), PC
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PC C12N5/00,(C12N5/00,C12R1:91)
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Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCTCATCGCCCC 15
Db 1 CCTCCACGCCCC 12
RESULT 56
BD001614
LOCUS BD001614 12 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001614
VERSION BD001614.1 GI:18626173
KEYWORDS JP 2000342286-A/345.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 345 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342286-A/345
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR

14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
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14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
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PI JAMES J HOLESEK, ANTHONY J MAMONE
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PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC A61P1/16,
PC A61P31/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12Q1/68, PC
(C12N15/09, C12R1:93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
C12R1:93)
CC
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
/organism='Artificial Sequence'.
FEATURES
source 1..12
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCTCATCGCCCC 15
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Db 1 CCTCCACGCCCC 12
RESULT 57
AR030034/c
LOCUS AR030034 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 223 from patent US 5861244.
ACCESSION AR030034
VERSION AR030034.1 GI:5943248
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 223 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 TCGCCCTTC 18
||| |||||
Db 10 TCCCCCTTC 1
RESULT 58
AR043160
LOCUS AR043160 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 44 from patent US 5814453.
ACCESSION AR043160
VERSION AR043160.1 GI:5964168
KEYWORDS .

SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Beck, J. Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 44 29-SEP-1998;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 TCATCGCCCC 15
| |||||
Db 1 TTATCGCCCC 10
RESULT 59
AR074660
LOCUS AR074660 10 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 44 from patent US 5955274.
ACCESSION AR074660
VERSION AR074660.1 GI:10001413
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ligon, J.M. and Beck, J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5955274-A 44 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 TCATCGCCCC 15
| |||||
Db 1 TTATCGCCCC 10
RESULT 60
BD238681/c
LOCUS BD238681 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238681
VERSION BD238681.1 GI:33048451
KEYWORDS JP 2002534056-A/99.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 99 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/99
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR


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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      10  CGCCCCCTTCC 19
Db      10  CTCCCCCTTC 1

RESULT 63
BD240380
LOCUS      BD240380              10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Preparation and use of superior vaccines.
ACCESSION      BD240380
VERSION      BD240380.1   GI:33050150
KEYWORDS      JP 2002534056-A/1798.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1   (bases 1 to 10)
Robertson,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1798 15-OCT-2002;
GENZYME CORP

COMMENT
OS      Homo sapiens (human)
PN      JP 2002534056-A/1798
PD      15-OCT-2002
PF      18-JUN-1999   JP 2000554749
PR      19-JUN-1998   US      60/090039,19-JUN-1998   US      60/090040 PR
19-JUN-1998   US      60/090041,19-JUN-1998   US      60/089853 PR
19-JUN-1998   US      60/089997,19-JUN-1998   US      60/090079 PR
19-JUN-1998   US      60/090035,19-JUN-1998   US      60/089993 PR
19-JUN-1998   US      60/089992,19-JUN-1998   US      60/090072 PR
19-JUN-1998   US      60/089878,19-JUN-1998   US      60/089991 PR
19-JUN-1998   US      60/090000,19-JUN-1998   US      60/090048 PR
19-JUN-1998   US      60/089999,19-JUN-1998   US      60/090043 PR
19-JUN-1998   US      60/090042,19-JUN-1998   US      60/090036 PR
19-JUN-1998   US      60/090044,19-JUN-1998   US      60/089844 PR
19-JUN-1998   US      60/090080,19-JUN-1998   US      60/089833 PR
19-JUN-1998   US      60/089994,19-JUN-1998   US      60/090077 PR
19-JUN-1998   US      60/090078,19-JUN-1998   US      60/090047 PR
19-JUN-1998   US      60/090076,19-JUN-1998   US      60/090045 PR
08-DEC-1998   US      60/111715
PI      BRUCE L ROBERTS,SRINIVAS SHANKARA
PC      C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC      C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC      C12N15/00,C12N5/00,C12N15/00
CC      Preparation and use of superior vaccines
FH      Key      Location/Qualifiers
FT      source      1..10
FT      /organism='Homo sapiens (human)'.

FEATURES
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1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      10  CGCCCCCTTCC 19
Db      1  CCCCCCTTCC 10

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      10  CGCCCCCTTCC 19
Db      1  CCCCCCTTCC 10
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      10  CGCCCCCTTCC 19
Db      1  CTCCCCCTTC 10

RESULT 64
CS052685
LOCUS      CS052685              10 bp      DNA      linear      PAT 23-MAR-2005
DEFINITION      Sequence 26 from Patent WO2005021796.
ACCESSION      CS052685
VERSION      CS052685.1   GI:61891480
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS      Aerssens,J., Athanasiou,M., Brain,C., Cohen,N., Dain,B.,
Denton,R.R., Judson,R.S., Ozdemir,V. and Reed,C.R.
TITLE      Chrna2 genetic markers associated with galantamine response
JOURNAL      Patent: WO 2005021796-A 26 10-MAR-2005;
GENAissance Pharmaceuticals, Inc. (US)
FEATURES
source
1..10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Reverse Primer Extension Oligo for Detecting
Alleles at PSS in Haplotypes Comprising Preferred
Embodiments of Response Markers I and Response Markers II"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      10  CGCCCCCTTCC 19
Db      1  CTCCCCCTTC 10

RESULT 65
E27859
LOCUS      E27859              10 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION      Method for testing resistance of rice against Nilaparvata lugens
Stal, DNA fragment and PCR marker.
ACCESSION      E27859
VERSION      E27859.1   GI:13018284
KEYWORDS      JP 1999206376-A/10.
SOURCE      unidentified
ORGANISM      unidentified
unclassified.
1   (bases 1 to 10)
Takamichi,T., Hitoshi,N., Takako,T. and Norikuni,S.
Method for testing resistance of rice against Nilaparvata lugens
Stal, DNA fragment and PCR marker
Patent: JP 1999206376-A 10 03-AUG-1999;
AICHI PREF
OS      Unidentified
PN      JP 1999206376-A/10
PD      03-AUG-1999
PF      22-JAN-1998   JP 1998010845
PR
PI      TAKAMICHI TOYAMA,HITOSHI NAKAMAE,TAKAKO TSUJI,NORIKUNI SAKA PC
C12N15/09,C12Q1/68,G01N33/50//(C12N15/09,C12R1:91),C12N15/00, PC
(C12N15/00,C12R1:91)
CC
FH      Key      Location/Qualifiers
FT      source      1..10
FT      /organism='Unidentified'.

FEATURES
source
1..10
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;
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QY 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10

RESULT 66
I22209
LOCUS I22209 linear PAT 07-OCT-1996
DEFINITION Sequence 23 from patent US 5527671.
ACCESSION I22209
VERSION I22209.1 GI:1602563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Li,K., Rouse,D.I. and German,T.L.
TITLE Assay for verticillium dahliae
JOURNAL Patent: US 5527671-A 23 18-JUN-1996;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10

RESULT 67
AX152425/c
LOCUS AX152425 linear PAT 22-JUN-2001
DEFINITION Sequence 340 from Patent WO0138577.
ACCESSION AX152425
VERSION AX152425.1 GI:14534076
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 340 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATCGC 12
Db 10 ACCTCACCGC 1

RESULT 68
AX152861/c
LOCUS AX152861 linear PAT 22-JUN-2001
DEFINITION Sequence 776 from Patent WO0138577.
ACCESSION AX152861
VERSION AX152861.1 GI:14534512
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 776 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTA 21
Db 10 CCCCATCCTA 1

RESULT 69
AX152959
LOCUS AX152959 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 874 from Patent WO0138577.
ACCESSION AX152959
VERSION AX152959.1 GI:14534610
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 874 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCT 20
Db 1 GCCCCTGCCT 10

RESULT 70
AX152960
LOCUS AX152960 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 875 from Patent WO0138577.
ACCESSION AX152960
VERSION AX152960.1 GI:14534611
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 875 31-MAY-2001;

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FEATURES
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      Location/Qualifiers
        1..10
          /organism="Homo sapiens"
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          /db_xref="taxon:9606"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches 9;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy 11 GCCCCTTCCT 20
    ||||| |||
Db 1 GCCCCTGCCT 10

RESULT 71
AX153190/c
LOCUS AX153190 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1105 from Patent WO0138577.
ACCESSION AX153190
VERSION AX153190.1 GI:14534841
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1105 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
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      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches 9;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy 4 CCTCATCGCC 13
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Db 10 CCTCATCACC 1

RESULT 72
AX302593/c
LOCUS AX302593 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 111 from Patent WO0175177.
ACCESSION AX302593
VERSION AX302593.1 GI:17383120
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 111 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
  source
    1..10
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
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Qy 11 GCCCCTTCCT 20
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Db 10 GCCCCTCCCT 1

RESULT 73
BD007795/c
LOCUS BD007795 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007795
VERSION BD007795.1 GI:18636168
KEYWORDS JP 2001069993-A/71.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 71 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/71
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
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    1..10
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 10;
Best Local Similarity 90.0%;   Pred. No. 66;
Matches 9;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy 10 CGCCCTTCC 19
    | |||||
Db 10 CTCCTTCC 1

RESULT 74
AR029871
LOCUS AR029871 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 60 from patent US 5861244.
ACCESSION AR029871
VERSION AR029871.1 GI:5943085
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 60 19-JAN-1999;
FEATURES
  source
    1..11
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match      32.3%;   Score 8.4;   DB 1;   Length 11;
Best Local Similarity 90.0%;   Pred. No. 73;
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCGCCCTTC 18
Db 2 TCTCCCTTC 11

RESULT 75
CQ832679
LOCUS CQ832679 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 50 from Patent WO2004059002.
ACCESSION CQ832679
VERSION CQ832679.1 GI:50832286
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 50 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCCCCTTCCT 20
Db 2 GGCCCTTCCT 11

RESULT 76
CQ832959/c
LOCUS CQ832959 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 330 from Patent WO2004059002.
ACCESSION CQ832959
VERSION CQ832959.1 GI:50832566
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 330 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CGCCCTTC 19
Db 10 CTCCCTTC 1
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RESULT 77
CQ833029/c
LOCUS CQ833029 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 400 from Patent WO2004059002.
ACCESSION CQ833029
VERSION CQ833029.1 GI:50832636
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 400 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
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Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 TCCTAGCAT 26
Db 11 TACTAGCAT 2

RESULT 78
CQ835576
LOCUS CQ835576 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 634 from Patent WO2004059001.
ACCESSION CQ835576
VERSION CQ835576.1 GI:50835110
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 634 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCCCTTCCT 20
Db 1 GCCCTGCCT 10

RESULT 79
CQ836387
LOCUS CQ836387 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1445 from Patent WO2004059001.
ACCESSION CQ836387
VERSION CQ836387.1 GI:50835921
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1445 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 90.0%; Pred. No. 73;
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Qy 11 GCCCCTTCCT 20
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Db 2 GGCCCTTCCT 11
RESULT 80
CQ836706/c
LOCUS CQ836706 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1764 from Patent WO2004059001.
ACCESSION CQ836706
VERSION CQ836706.1 GI:50836240
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1764 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 15 CTTCCTAAGC 24
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Db 11 CATCCTAAGC 2
RESULT 81
CQ836926
LOCUS CQ836926 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1984 from Patent WO2004059001.
ACCESSION CQ836926
VERSION CQ836926.1 GI:50836460
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,

Conradt,M. and Hofmann,K.
Method for determining markers of human facial skin
Patent: WO 2004059001-A 1984 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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Best Local Similarity 90.0%; Pred. No. 73;
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Qy 5 CTCATCGCCC 14
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Db 1 CTCACCGCCC 10
RESULT 82
CQ836928
LOCUS CQ836928 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1986 from Patent WO2004059001.
ACCESSION CQ836928
VERSION CQ836928.1 GI:50836462
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1986 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 GCCCCTTCCT 20
| |||||
Db 2 GGCCCTTCCT 11
RESULT 83
CQ836982/c
LOCUS CQ836982 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2040 from Patent WO2004059001.
ACCESSION CQ836982
VERSION CQ836982.1 GI:50836516
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2040 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"

LOCUS AX393137 11 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 67 from Patent WO0210217.
ACCESSION AX393137
VERSION AX393137.1 GI:19701187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 67 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 15 CTTCCCTAAGC 24
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Db 11 CATCCTAAGC 2
RESULT 89
AX470453/c
LOCUS AX470453 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 30 from Patent WO02053773.
ACCESSION AX470453
VERSION AX470453.1 GI:22205578
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 30 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 CCCCTTCCTA 21
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Db 10 CCCCATCCTA 1
RESULT 90
AX470489/c
LOCUS AX470489 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 66 from Patent WO02053773.
ACCESSION AX470489
VERSION AX470489.1 GI:22205614
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 66 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 GCCCCTTCCT 20
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Db 10 GCCCCTTCCT 1
RESULT 91
AX470678/c
LOCUS AX470678 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 255 from Patent WO02053773.
ACCESSION AX470678
VERSION AX470678.1 GI:22205803
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 255 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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/db_xref="taxon:9606"
Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 CCTCATCGCC 13
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Db 10 CCTCATCTCC 1
RESULT 92
AX471686/c
LOCUS AX471686 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1263 from Patent WO02053773.
ACCESSION AX471686
VERSION AX471686.1 GI:22206811
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1263 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"

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Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATCGCC 13
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Db      10 CCTCATCACC 1

RESULT 93
AX623151/c
LOCUS      AX623151      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 192 from Patent WO02053774.
ACCESSION  AX623151
VERSION    AX623151.1 GI:28451092
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 192 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 TTCCTAAGCA 25
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Db      10 TTCCTAGGCA 1

RESULT 94
AX625223/c
LOCUS      AX625223      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2264 from Patent WO02053774.
ACCESSION  AX625223
VERSION    AX625223.1 GI:28453164
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 2264 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Query Match      32.3%; Score 8.4; DB 1; Length 11;
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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GCCCCCTTCCT 20
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Db      10 GCCCCTCCCT 1

RESULT 95
AX625417/c
LOCUS      AX625417      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2458 from Patent WO02053774.
ACCESSION  AX625417
VERSION    AX625417.1 GI:28453358
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 2458 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATCGCC 13
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Db      10 CCTCATCTCC 1

RESULT 96
AX626288
LOCUS      AX626288      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3329 from Patent WO02053774.
ACCESSION  AX626288
VERSION    AX626288.1 GI:28454326
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 3329 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CTCATCGCCC 14
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Db      1 CTCACCGCCC 10

RESULT 97
AX626376
LOCUS      AX626376      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3417 from Patent WO02053774.
ACCESSION  AX626376
VERSION    AX626376.1 GI:28454414

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KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3417 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 GCCCCTTCCT 20
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Db      2 GCCCCTCCCT 11

RESULT 98
AX627454/c
LOCUS      AX627454
DEFINITION Sequence 4495 from Patent WO02053774.
ACCESSION  AX627454
VERSION     AX627454.1 GI:28455492
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4495 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 GCCCCTTCCT 20
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Db      2 GCCCCTCCCT 11

RESULT 99
AX627875/c
LOCUS      AX627875
DEFINITION Sequence 4916 from Patent WO02053774.
ACCESSION  AX627875
VERSION     AX627875.1 GI:28455913
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
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JOURNAL     Patent: WO 02053774-A 4916 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACCTCATC 10
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Db      10 CCACCTCCTC 1

RESULT 100
AX628365
LOCUS      AX628365
DEFINITION Sequence 5406 from Patent WO02053774.
ACCESSION  AX628365
VERSION     AX628365.1 GI:28456403
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5406 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 GCCCCTTCCT 20
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Db      1 GCCCCTGCCT 10

RESULT 101
AX628882
LOCUS      AX628882
DEFINITION Sequence 5923 from Patent WO02053774.
ACCESSION  AX628882
VERSION     AX628882.1 GI:28456920
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5923 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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Query Match      32.3%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 GCCCCTTCCT 20
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Db      1 GCCCCTGCCT 10

RESULT 101
AX628882
LOCUS      AX628882
DEFINITION Sequence 5923 from Patent WO02053774.
ACCESSION  AX628882
VERSION     AX628882.1 GI:28456920
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5923 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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Query Match      32.3%; Score 8.4; DB 1; Length 11;
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCT 20 11 bp DNA linear PAT 21-FEB-2003
| | | | |
Db 2 GCGCCTTCCT 11

RESULT 102
AX629566/c
LOCUS AX629566 6607 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6607 from Patent WO02053774.
ACCESSION AX629566
VERSION AX629566.1 GI:28457604
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6607 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCC 15
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Db 11 TCATCTCCCC 2

RESULT 103
AX629571
LOCUS AX629571 6612 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6612 from Patent WO02053774.
ACCESSION AX629571
VERSION AX629571.1 GI:28457609
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6612 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCT 20
| | | | |
Db 2 GCGCCTTCCT 11

RESULT 104

AX629791/c
LOCUS AX629791 6832 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6832 from Patent WO02053774.
ACCESSION AX629791
VERSION AX629791.1 GI:28457829
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6832 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCC 13
| | | | |
Db 10 CCTCATCACC 1

RESULT 105
AX630124/c
LOCUS AX630124 7165 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7165 from Patent WO02053774.
ACCESSION AX630124
VERSION AX630124.1 GI:28458162
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7165 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTA 21
| | | | |
Db 10 CCCCATCCTA 1

RESULT 106
AX630572/c
LOCUS AX630572 7613 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7613 from Patent WO02053774.
ACCESSION AX630572
VERSION AX630572.1 GI:28458610
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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REFERENCE
AUTHORS      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE         Hominidae; Homo.
JOURNAL       Petersohn,D., Conradt,M. and Hofmann,K.
               Method for determining homeostasis of the skin
               Patent: WO 02053774-A 7613 11-JUL-2002;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      Location/Qualifiers
               1. .11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGCA 25
Db 10 TTCCTAGGCA 1

RESULT 107
AX632644/c
LOCUS AX632644 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9686 from Patent WO02053774.
ACCESSION AX632644
VERSION AX632644.1 GI:28468259
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9686 11-JUL-2002;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCT 20
Db 10 GCCCCTCCCT 1

RESULT 108
A61526/c
LOCUS A61526 12 bp DNA linear PAT 09-MAR-1998
DEFINITION Sequence 95 from Patent WO9710332.
ACCESSION A61526
VERSION A61526.1 GI:3715897
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
           unclassified sequences.

REFERENCE 1
AUTHORS Schmidt,G.
TITLE CHIMAERIC OLIGONUCLEOTIDES AND USES THEREOF IN THE IDENTIFICATION
           OF ANTISENSE BINDING SITES
JOURNAL Patent: WO 9710332-A 95 20-MAR-1997;
           BRAX GENOMICS LTD (GB)
FEATURES Location/Qualifiers
               1. .12
               /organism="unidentified"
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REFERENCE
AUTHORS      /mol_type="unassigned DNA"
TITLE         /db_xref="taxon:32644"
JOURNAL       Query Match      32.3%; Score 8.4; DB 1; Length 12;
               Best Local Similarity 90.0%; Pred. No. 80;
               Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CCTTCCTAAG 23
Db 10 CTTTCCTAAG 1

RESULT 109
A95406
LOCUS A95406 12 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 13 from Patent WO9927086.
ACCESSION A95406
VERSION A95406.1 GI:6779450
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
           unclassified sequences.

REFERENCE 1 (bases 1 to 12)
AUTHORS Thompson,A.H. and Schmidt,G.
TITLE CHIMERIC ANTISENSE OLIGONUCLEOTIDES AGAINST TNF-ALPHA AND THEIR
           USES
JOURNAL Patent: WO 9927086-A 13 03-JUN-1999;
           BRAX GENOMICS LTD (GB); THOMPSON ANDREW HUGIN (GB)
FEATURES Location/Qualifiers
               1. .12
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match      32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CCTTCCTAAG 23
Db 3 CTTTCCTAAG 12

RESULT 110
AR058757/c
LOCUS AR058757 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 334 from patent US 5837832.
ACCESSION AR058757
VERSION AR058757.1 GI:5984334
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
           Unclassified.

REFERENCE 1 (bases 1 to 12)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
           Lipshutz,R.J., Lobb,R.P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 334 17-NOV-1998;
           Location/Qualifiers
           source
           1. .12
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 TCCTAAGCAT 26
Db 11 TCCTCAGCAT 2

RESULT 111
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CQ766296
LOCUS CQ766296 12 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 257 from Patent WO2004005547.
ACCESSION CQ766296
VERSION CQ766296.1 GI:44908556
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weinzierl,R.
TITLE Method
JOURNAL Patent: WO 2004005547-A 257 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
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1. .12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HS motif"
Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACCTCATC 10
|||||
Db 3 CCACCTCAGC 12
RESULT 112
AR199106/c
LOCUS AR199106 12 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 54 from patent US 6355418.
ACCESSION AR199106
VERSION AR199106.1 GI:20249180
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Schmidt,G.
TITLE Chimeric oligonucleotides and uses thereof in the identification of antisense binding sites
JOURNAL Patent: US 6355418-A 54 12-MAR-2002;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 CCTTCCTAAG 23
|||||
Db 10 CTTTCCTAAG 1
RESULT 113
AR408041/c
LOCUS AR408041 12 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 134 from patent US 6632057.
ACCESSION AR408041
VERSION AR408041.1 GI:40158028
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 134 14-OCT-2003;

GFI Aerospace; Paris;
FRX;
FEATURES
source
Location/Qualifiers
1. .12
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CTTCCTAAGC 24
|||||
Db 12 CTTCCTAGGC 3
RESULT 114
AX467018/c
LOCUS AX467018 12 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 47 from Patent WO0224950.
ACCESSION AX467018
VERSION AX467018.1 GI:21900359
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Liang,Z., Zhang,H.Y. and Wahlestedt,C.
TITLE Methods and means of rna analysis
JOURNAL Patent: WO 0224950-A 47 28-MAR-2002;
Neuromics Inc. (US)
FEATURES
source
1. .12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetically generated oligonucleotide"
Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACCTCATC 10
|||||
Db 12 CCACCGCATC 3
RESULT 115
AR121979
LOCUS AR121979 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 16 from patent US 6160202.
ACCESSION AR121979
VERSION AR121979.1 GI:14105555
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Bustos,M.M. and Chern,M.-S.
TITLE Modification of seed crops with transcription factors
JOURNAL Patent: US 6160202-A 16 12-DEC-2000;
FEATURES
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACCTCA 8
|||||
Db 2 CCACCTCA 9

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 10)
TITLE Roberts,B.L. and Shankara,S.
JOURNAL Preparation and use of superior vaccines
Patent: JP 2002534056-A 1437 15-OCT-2002;
GENZYME CORP

COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1437
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCA 8
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Db 3 CCACCTCA 10

RESULT 123
E07298
LOCUS E07298
DEFINITION Oligonucleotides of lettuce's DNA linear PAT 29-SEP-1997
ACCESSION E07298
VERSION E07298.1 GI:2175439
KEYWORDS JP 1994113849-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Yamamoto,T. and Nishikawa,A.
TITLE METHOD FOR DISTINGUISHING VARIETY OF LETTUCE USING OLIGONUCLEOTIDE AND ITS OLIGONUCLEOTIDE
JOURNAL Patent: JP 1994113849-A 1 26-APR-1994;
SUMITOMO CHEM CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994113849-A/1
PD 26-APR-1994
PF 09-OCT-1992 JP 1992271760
PI YAMAMOTO TOSHIYA, NISHIKAWA AKIRA
PC C12N15/11,C12Q1/68,G01N33/48,G01N33/48;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1..10
FT /organism='Artificial sequences'.
FEATURES source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TCCTAAGC 24
|||||
Db 3 TCCTAAGC 10

RESULT 124
E07306
LOCUS E07306
DEFINITION Oligonucleotide of rice plant's DNA linear PAT 29-SEP-1997
ACCESSION E07306
VERSION E07306.1 GI:2175447
KEYWORDS JP 1994113850-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Yamamoto,T. and Nishikawa,A.
TITLE METHOD FOR DISTINGUISHING VARIETY OF RICE PLANT USING OLIGONUCLEOTIDE AND ITS OLIGONUCLEOTIDE
JOURNAL Patent: JP 1994113850-A 1 26-APR-1994;
SUMITOMO CHEM CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994113850-A/1
PD 26-APR-1994
PF 09-OCT-1992 JP 1992271760
PI YAMAMOTO TOSHIYA, NISHIKAWA AKIRA
PC C12N15/11,C12Q1/68,G01N33/48,G01N33/48;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1..10
FT /organism='Artificial sequences'.
FEATURES source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TCCTAAGC 24
|||||
Db 3 TCCTAAGC 10

RESULT 125
E39656/c

PI YAMAMOTO TOSHIYA, NISHIKAWA AKIRA
PC C12N15/11,C12Q1/68,G01N33/48,G01N33/48;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1..10
FT /organism='Artificial sequences'.
FEATURES source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TCCTAAGC 24
|||||
Db 3 TCCTAAGC 10

RESULT 124
E07306
LOCUS E07306
DEFINITION Oligonucleotide of rice plant's DNA linear PAT 29-SEP-1997
ACCESSION E07306
VERSION E07306.1 GI:2175447
KEYWORDS JP 1994113850-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Yamamoto,T. and Nishikawa,A.
TITLE METHOD FOR DISTINGUISHING VARIETY OF RICE PLANT USING OLIGONUCLEOTIDE AND ITS OLIGONUCLEOTIDE
JOURNAL Patent: JP 1994113850-A 1 26-APR-1994;
SUMITOMO CHEM CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994113850-A/1
PD 26-APR-1994
PF 09-OCT-1992 JP 1992271760
PI YAMAMOTO TOSHIYA, NISHIKAWA AKIRA
PC C12N15/11,C12Q1/68,G01N33/48,G01N33/48;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1..10
FT /organism='Artificial sequences'.
FEATURES source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TCCTAAGC 24
|||||
Db 3 TCCTAAGC 10

RESULT 125
E39656/c

LOCUS E39656 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39656
VERSION E39656.1 GI:18621747
KEYWORDS JP 2000279181-A/189.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 189 10-OCT-2000;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2000279181-A/189
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR
PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CCCCTTCC 19
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Db 8 CCCCTTCC 1
RESULT 126
AR561756/c
LOCUS AR561756 10 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 20 from patent US 6759195.
ACCESSION AR561756
VERSION AR561756.1 GI:53975407
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Bentley,W.E. and Gill,R.
TITLE Method of differential display of prokaryotic messenger RNA by RTPCR
JOURNAL Patent: US 6759195-A 20 06-JUL-2004;
University of Maryland Biotechnology Institute; Baltimore, MD
FEATURES
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/organism='unknown'
/mol_type='genomic DNA'
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TCATCGCC 13
|||||
Db 10 TCATCGCC 3
RESULT 127
AR575231

LOCUS AR575231 10 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 69 from patent US 6770738.
ACCESSION AR575231
VERSION AR575231.1 GI:56576127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Mollegaard,N.E.
TITLE Higher order structure and binding of peptide nucleic acids
JOURNAL Patent: US 6770738-A 69 03-AUG-2004;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
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1..10
/organism='unknown'
/mol_type='genomic DNA'
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 CCCTTCCT 20
|||||
Db 1 CCCTTCCT 8
RESULT 128
AX467563
LOCUS AX467563 10 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 2 from Patent WO0218607.
ACCESSION AX467563
VERSION AX467563.1 GI:21900758
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Conkling,M.A. and Li,Y.
TITLE Transgenic plants containing molecular decoys that alter protein content therein
JOURNAL Patent: WO 0218607-A 2 07-MAR-2002;
NORTH CAROLINA STATE UNIVERSITY (US)
FEATURES
source
1..10
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Synthetic oligonucleotide'
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Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACCTCA 8
|||||
Db 2 CCACCTCA 9
RESULT 129
BD007786/c
LOCUS BD007786 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007786
VERSION BD007786.1 GI:18636159
KEYWORDS JP 2001069993-A/62.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)

AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 62 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/62
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
/organism='Homo sapiens (human)'.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 CCCCTTCC 19
|||||
Db 9 CCCCTTCC 2
RESULT 130
A15322
LOCUS A15322 11 bp DNA linear PAT 23-MAR-1994
DEFINITION Oligonucleotide Cd8.
ACCESSION A15322
VERSION A15322.1 GI:512136
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 11)
AUTHORS Ueda,I., Niwa,M., Saito,Y., Yamada,H. and Ishii,Y.
TITLE A process for the production of alpha-human atrial natriuretic polypeptide
JOURNAL Patent: EP 0206769-A 61 30-DEC-1986;
FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES
source 1..11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TCATCGCC 13
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Db 4 TCATCGCC 11
RESULT 131
A16522
LOCUS A16522 11 bp DNA linear PAT 17-MAR-1994
DEFINITION oligonucleotide Cd8.
ACCESSION A16522
VERSION A16522.1 GI:489910
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 11)
AUTHORS Ueda,I., Niwa,M., Saito,Y., Yamada,H. and Ishii,Y.
TITLE A process for the production of alpha-human atrial natriuretic polypeptide
JOURNAL Patent: EP 0440311-A 78 07-AUG-1991;
FUJISAWA PHARMACEUTICAL CO., LTD
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source 1..11
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/db_xref="taxon:32630"
Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TCATCGCC 13
|||||
Db 4 TCATCGCC 11
RESULT 132
AR004550
LOCUS AR004550 11 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 9 from patent US 5747253.
ACCESSION AR004550
VERSION AR004550.1 GI:3965429
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Ecker,D.J., Vickers,T. and Davis,P.
TITLE Combinatorial oligomer immunoabsorbant screening assay for transcription factors and other biomolecule binding
JOURNAL Patent: US 5747253-A 9 05-MAY-1998;
FEATURES
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 CCCTTCCT 20
|||||
Db 1 CCCTTCCT 8
RESULT 133
AR032093
LOCUS AR032093 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5866698.
ACCESSION AR032093
VERSION AR032093.1 GI:5946382
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Ecker,D., Vickers,T.A. and Bruice,T.W.
TITLE Modulation of gene expression through interference with RNA secondary structure
JOURNAL Patent: US 5866698-A 14 02-FEB-1999;
FEATURES
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCT 20
Db 1 CCCTTCCT 8

RESULT 134
CQ828745
LOCUS 11 bp DNA PAT 05-JUL-2004
DEFINITION Sequence 463 from Patent WO2004053120.
ACCESSION CQ828745
VERSION CQ828745.1 GI:49732228
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 463 24-JUN-2004;
Gruenthal GmbH (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
/note="V\$DELTAEF1 01"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCAT 9
Db 4 CACCTCAT 11

RESULT 135
CQ833719
LOCUS 11 bp DNA PAT 29-JUL-2004
DEFINITION Sequence 1090 from Patent WO2004059002.
ACCESSION CQ833719
VERSION CQ833719.1 GI:50833326
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 1090 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTCCTAAG 23
Db 4 TTCCTAAG 11

RESULT 136

CQ835404/c
LOCUS 11 bp DNA PAT 29-JUL-2004
DEFINITION Sequence 462 from Patent WO2004059001.
ACCESSION CQ835404
VERSION CQ835404.1 GI:50834938
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 462 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCA 8
Db 10 CCACCTCA 3

RESULT 137
CQ835452
LOCUS 11 bp DNA PAT 29-JUL-2004
DEFINITION Sequence 510 from Patent WO2004059001.
ACCESSION CQ835452
VERSION CQ835452.1 GI:50834986
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 510 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCT 20
Db 3 CCCTTCCT 10

RESULT 138
CQ837286/c
LOCUS 11 bp DNA PAT 29-JUL-2004
DEFINITION Sequence 2344 from Patent WO2004059001.
ACCESSION CQ837286
VERSION CQ837286.1 GI:50836820
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

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ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2344 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 CGCCCCCTT 17
        |||||
Db      8 CGCCCCCTT 1

RESULT 139
CQ837568
LOCUS      CQ837568
DEFINITION Sequence 2626 from Patent WO2004059001.
ACCESSION  CQ837568
VERSION    CQ837568.1 GI:50837102
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2626 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15 CTTCTCTAA 22
        |||||
Db      3 CTTCTCTAA 10

RESULT 140
CQ838068
LOCUS      CQ838068
DEFINITION Sequence 3126 from Patent WO2004059001.
ACCESSION  CQ838068
VERSION    CQ838068.1 GI:50837602
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
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TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 3126 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
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              /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 CCTTCCTA 21
        |||||
Db      2 CCTTCCTA 9

RESULT 141
CQ838137/c
LOCUS      CQ838137
DEFINITION Sequence 3195 from Patent WO2004059001.
ACCESSION  CQ838137
VERSION    CQ838137.1 GI:50837671
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 3195 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CACCTCAT 9
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Db      9 CACCTCAT 2

RESULT 142
CS058235
LOCUS      CS058235
DEFINITION Sequence 132 from Patent WO2005028671.
ACCESSION  CS058235
VERSION    CS058235.1 GI:62551418
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS      Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
              Kessler-Becker,D.
TITLE        Method for determining hair cycle markers
JOURNAL      Patent: WO 2005028671-A 132 31-MAR-2005;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
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/db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ATCGCCCC 15
Db      4 ATCGCCCC 11

RESULT 143
I67665
LOCUS      I67665
DEFINITION Sequence 9 from patent US 5672472.
ACCESSION  I67665
VERSION    I67665.1 GI:2731200
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11)
AUTHORS    Ecker,D.J., Wyatt,J., Bruice,T.W., Anderson,K., Hanecak,R.C.,
            Vickers,T. and Davis,P.
TITLE      Synthetic unrandomization of oligomer fragments
JOURNAL    Patent: US 5672472-A 9 30-SEP-1997;
FEATURES   Location/Qualifiers
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            1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCT 20
Db      1 CCCTTCCT 8

RESULT 144
I85557
LOCUS      I85557
DEFINITION Sequence 9 from patent US 5698391.
ACCESSION  I85557
VERSION    I85557.1 GI:3205275
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11)
AUTHORS    Cook,P.Dan., Ecker,D.J., Wyatt,J., Bruice,T.W., Anderson,K.,
            Hanecak,R., Vickers,T., Davis,P., Freier,S.M., Sanghvi,Y.S. and
            Brown-Driver,V.
TITLE      Methods for synthetic unrandomization of oligomer fragments
JOURNAL    Patent: US 5698391-A 9 16-DEC-1997;
FEATURES   Location/Qualifiers
            source
            1. .11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCT 20
Db      1 CCCTTCCT 8

RESULT 145
AX471421/c
LOCUS      AX471421
DEFINITION Sequence 9 from patent US 5698391.
ACCESSION  AX471421
VERSION    AX471421.1 GI:22053773
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 11)
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
            Method for determining skin stress or skin ageing in vitro
TITLE      Patent: WO 02053773-A 9 11-JUL-2002;
JOURNAL    HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source
            1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
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DEFINITION Sequence 998 from Patent WO02053773.
ACCESSION  AX471421
VERSION    AX471421.1 GI:22206546
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
            Method for determining skin stress or skin ageing in vitro
TITLE      Patent: WO 02053773-A 998 11-JUL-2002;
JOURNAL    HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source
            1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
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Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TCCTAAGC 24
Db      11 TCCTAAGC 4

RESULT 146
AX471761
LOCUS      AX471761
DEFINITION Sequence 1338 from Patent WO02053773.
ACCESSION  AX471761
VERSION    AX471761.1 GI:22206886
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
            Method for determining skin stress or skin ageing in vitro
TITLE      Patent: WO 02053773-A 1338 11-JUL-2002;
JOURNAL    HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source
            1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
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Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCC 19
Db      4 CCCCTTCC 11

RESULT 147
AX623532/c
LOCUS      AX623532
DEFINITION Sequence 573 from Patent WO02053774.
ACCESSION  AX623532
VERSION    AX623532.1 GI:28451473
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
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REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 573 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1
      /db_xref="taxon:9606"
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  2 CACCTCAT 9
    |||||
  9 CACCTCAT 2

Db

RESULT 148
AX623940/c
LOCUS      AX623940
DEFINITION Sequence 981 from Patent WO02053774.
ACCESSION  AX623940
VERSION     AX623940.1 GI:28451881
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 981 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1
      /db_xref="taxon:9606"
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  10 CGCCCCCT 17
    |||||
  8 CGCCCCCT 1

Db

RESULT 149
AX624535
LOCUS      AX624535
DEFINITION Sequence 1576 from Patent WO02053774.
ACCESSION  AX624535
VERSION     AX624535.1 GI:28452476
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 1576 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1
      /db_xref="taxon:9606"
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
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/db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  8 ATGCCCCC 15
    |||||
  4 ATGCCCCC 11

Db

RESULT 150
AX624841/c
LOCUS      AX624841
DEFINITION Sequence 1882 from Patent WO02053774.
ACCESSION  AX624841
VERSION     AX624841.1 GI:28452782
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 1882 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1
      /db_xref="taxon:9606"
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  17 TCCTAAGC 24
    |||||
  11 TCCTAAGC 4

Db

RESULT 151
AX626013
LOCUS      AX626013
DEFINITION Sequence 3054 from Patent WO02053774.
ACCESSION  AX626013
VERSION     AX626013.1 GI:28454051
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 3054 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source
    1
      /db_xref="taxon:9606"
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  15 CTTCTTAA 22
    |||||
  3 CTTCTTAA 10

Db
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RESULT 152
AX626608
LOCUS AX626608 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3649 from Patent WO02053774.
ACCESSION AX626608
VERSION AX626608.1 GI:28454646
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3649 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 CCCTTCCT 20
Db 3 CCCTTCCT 10
RESULT 153
AX628205/c
LOCUS AX628205 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5246 from Patent WO02053774.
ACCESSION AX628205
VERSION AX628205.1 GI:28456243
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5246 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 CCTTCCTA 21
Db 11 CCTTCCTA 4
RESULT 154
AX628339
LOCUS AX628339 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5380 from Patent WO02053774.
ACCESSION AX628339
VERSION AX628339.1 GI:28456377
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5380 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACCTCA 8
Db 4 CCACCTCA 11
RESULT 155
AX629051
LOCUS AX629051 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6092 from Patent WO02053774.
ACCESSION AX629051
VERSION AX629051.1 GI:28457089
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6092 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 CCTTCCTA 21
Db 2 CCTTCCTA 9
RESULT 156
AX630007
LOCUS AX630007 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7048 from Patent WO02053774.
ACCESSION AX630007
VERSION AX630007.1 GI:28458045
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7048 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

LOCUS AR024154 11 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 104 from patent US 5795778.
ACCESSION AR024154
VERSION AR024154.1 GI:3977448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 5795778-A 104 18-AUG-1998;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCCCTTCCT 20
| | | | | | | |
Db 1 CCCCCCTGCCT 11

RESULT 162
LOCUS AR030166 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 355 from patent US 5861244.
ACCESSION AR030166
VERSION AR030166.1 GI:5943380
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 355 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15
| | | | | | | |
Db 1 CTCCTCTCCCC 11

RESULT 163
LOCUS BD124409/c 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124409
VERSION BD124409.1 GI:23219354
KEYWORDS JP 2002503460-A/240.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 240 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/240

PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1..11
FT /organism="Mus musculus (mouse)".
FEATURES Location/Qualifiers
source 1..11
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCTTAAGCA 25
| | | | | | | |
Db 11 CATCATAGCA 1

RESULT 164
LOCUS CQ832668 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 39 from Patent WO2004059002.
ACCESSION CQ832668
VERSION CQ832668.1 GI:50832275
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 39 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
| | | | | | | |
Db 1 CCCCCACCTAA 11

RESULT 165
LOCUS CQ833592 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 963 from Patent WO2004059002.
ACCESSION CQ833592
VERSION CQ833592.1 GI:50833199
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,

Conradt,M. and Hofmann,K.
Method for determining the homeostasis of hairy skin
Patent: WO 2004059002-A 963 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCATCGCCCC 15 11 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION
Sequence 961 from Patent WO2004059001.
ACCESSION
CQ835903
VERSION
CQ835903.1 GI:50835437
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 961 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCATCGCCCC 15 11 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION
Sequence 961 from Patent WO2004059001.
ACCESSION
CQ835903
VERSION
CQ835903.1 GI:50835437
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 961 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCTCATCGCCC 14 11 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION
Sequence 1255 from Patent WO2004059001.
ACCESSION
CQ836197
VERSION
CQ836197.1 GI:50835731
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 1255 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CCCCTTCCTAA 22 11 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION
Sequence 1867 from Patent WO2004059001.
ACCESSION
CQ836809
VERSION
CQ836809.1 GI:50836343
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 1867 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCC 19 11 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION
Sequence 2818 from Patent WO2004059001.
ACCESSION
CQ837760
VERSION
CQ837760.1 GI:50837294
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 2818 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCC 19 11 bp DNA linear PAT 29-JUL-2004
LOCUS
DEFINITION
Sequence 2818 from Patent WO2004059001.
ACCESSION
CQ837760
VERSION
CQ837760.1 GI:50837294
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 2818 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
Db 1 CGCCGCTTCT 11

RESULT 170
CQ838066/c
LOCUS CQ838066 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 3124 from Patent WO2004059001.
ACCESSION CQ838066
VERSION CQ838066.1 GI:50837600
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 3124 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TCATCGCCCT 16
Db 11 TCTGCGCCCT 1

RESULT 171
CS086765/c
LOCUS CS086765 11 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 14 from Patent WO2005042018.
ACCESSION CS086765
VERSION CS086765.1 GI:66712216
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Uhlmann,E., Vollmer,J., Krieg,A.M. and Noll,B.O.
TITLE C-class oligonucleotide analogs with enhanced immunostimulatory potency
JOURNAL Patent: WO 2005042018-A 14 12-MAY-2005;
Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc. (US)

FEATURES
source Location/Qualifiers
1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCC 13
Db 11 ACCTCCTCGAC 1

RESULT 172
AR224372

LOCUS AR224372 11 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 104 from patent US 6440719.
ACCESSION AR224372
VERSION AR224372.1 GI:23333149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 6440719-A 104 27-AUG-2002;
Ribozyme Pharmaceuticals, Inc.; Boulder, CO

FEATURES
source Location/Qualifiers
1. .11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
Db 1 CCCCCCTGCCT 11

RESULT 173
AR301659/c
LOCUS AR301659 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 240 from patent US 6538173.
ACCESSION AR301659
VERSION AR301659.1 GI:31689461
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 240 25-MAR-2003;
The Wistar Institute; Philadelphia, PA;
WOX;

FEATURES
source Location/Qualifiers
1. .11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCTAAGCA 25
Db 11 CATCATAAGCA 1

RESULT 174
AR365391/c
LOCUS AR365391 11 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 21 from patent US 5494663.
ACCESSION AR365391
VERSION AR365391.1 GI:34428970
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Yamada,M., Furutani,Y., Yamayoshi,M., Notake,M. and Yamagishi,J.
TITLE Treatment of microbial infection with interleukin 1 polypeptides
JOURNAL Patent: US 5494663-A 21 27-FEB-1996;
Dainippon Pharmaceutical Co., Ltd.; Osaka; JPX;

ACCESSION AX624516
VERSION AX624516.1 GI:28452457
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1557 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CACCTCATCGC 12
|||||
Db 1 CACCCCTCGC 11
RESULT 180
AX624591/c
LOCUS AX624591 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1632 from Patent WO02053774.
ACCESSION AX624591
VERSION AX624591.1 GI:28452532
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1632 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 15 CTTCTTAAGCA 25
|||||
Db 11 CTTCCGCAGCA 1
RESULT 181
AX624873/c
LOCUS AX624873 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1914 from Patent WO02053774.
ACCESSION AX624873
VERSION AX624873.1 GI:28452814
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1914 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 ATGCGCCCTTC 18
|||||
Db 11 AGCACCCCTTC 1
RESULT 182
AX625228
LOCUS AX625228 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2269 from Patent WO02053774.
ACCESSION AX625228
VERSION AX625228.1 GI:28453169
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2269 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 CCCCTTCCTAA 22
|||||
Db 1 CCCCCACCTAA 11
RESULT 183
AX625386
LOCUS AX625386 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2427 from Patent WO02053774.
ACCESSION AX625386
VERSION AX625386.1 GI:28453327
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2427 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15
Db 1 CTCAACCCCCC 11

RESULT 184
AX625728/c
LOCUS AX625728 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2769 from Patent WO02053774.
ACCESSION AX625728
VERSION AX625728.1 GI:28453669
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2769 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TCGCCCCCTTCC 19
Db 11 TCGACCCCTGCC 1

RESULT 185
AX625963
LOCUS AX625963 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3004 from Patent WO02053774.
ACCESSION AX625963
VERSION AX625963.1 GI:28454001
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3004 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCTTAAGCA 25
Db 1 CTTCATAACCA 11

RESULT 186
AX626384/c
LOCUS AX626384 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3425 from Patent WO02053774.
ACCESSION AX626384
VERSION AX626384.1 GI:28454422
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3425 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCG 11
Db 11 CCTCCTCGTCG 1

RESULT 187
AX627272/c
LOCUS AX627272 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4313 from Patent WO02053774.
ACCESSION AX627272
VERSION AX627272.1 GI:28455310
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4313 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 TTCCTAAGCAT 26
Db 11 TTCCTCAGCCT 1

RESULT 188
AX627387
LOCUS AX627387 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4428 from Patent WO02053774.
ACCESSION AX627387
VERSION AX627387.1 GI:28455425
KEYWORDS .
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4428 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCTCATCGCCC 14
|||||
Db 1 CCTCATTTCCC 11
RESULT 189
AX627599/c
LOCUS AX627599 11 bp DNA PAT 21-FEB-2003
DEFINITION Sequence 4640 from Patent WO02053774.
ACCESSION AX627599
VERSION AX627599.1 GI:28455637
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4640 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 CCCCTTCCTAA 22
|||||
Db 11 CTCCTCCCTAA 1
RESULT 190
AX628049
LOCUS AX628049 11 bp DNA PAT 21-FEB-2003
DEFINITION Sequence 5090 from Patent WO02053774.
ACCESSION AX628049
VERSION AX628049.1 GI:28456087
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5090 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 CCCCTTCCTAA 22
|||||
Db 1 CCCCTTCCTTA 11
RESULT 191
AX628099/c
LOCUS AX628099 11 bp DNA PAT 21-FEB-2003
DEFINITION Sequence 5140 from Patent WO02053774.
ACCESSION AX628099
VERSION AX628099.1 GI:28456137
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5140 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 TCATCGCCCT 16
|||||
Db 11 TCCTCTCCCT 1
RESULT 192
AX628377/c
LOCUS AX628377 11 bp DNA PAT 21-FEB-2003
DEFINITION Sequence 5418 from Patent WO02053774.
ACCESSION AX628377
VERSION AX628377.1 GI:28456415
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5418 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TCATCGCCCT 16
Db 11 TCTGCGCCCT 1

RESULT 193
AX628495/c

LOCUS AX628495 11 bp DNA linear PAT 21-FEB-2003

DEFINITION Sequence 5536 from Patent WO02053774.

ACCESSION AX628495

VERSION AX628495.1 GI:28456533

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 5536 11-JUL-2002;

JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers

source 1..11

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 96;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCATCGCCCC 15
Db 11 CTGATCGCCTC 1

RESULT 194
AX629144

LOCUS AX629144 11 bp DNA linear PAT 21-FEB-2003

DEFINITION Sequence 6185 from Patent WO02053774.

ACCESSION AX629144

VERSION AX629144.1 GI:28457182

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 6185 11-JUL-2002;

JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers

source 1..11

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 96;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CGCCCCCTTCTT 20
Db 1 CGCCGCTTCTT 11

RESULT 195
AX629301/c

LOCUS AX629301 11 bp DNA linear PAT 21-FEB-2003

DEFINITION Sequence 6808 from Patent WO02053774.

ACCESSION AX629767

VERSION AX629767.1 GI:28457805

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

DEFINITION Sequence 6342 from Patent WO02053774.

ACCESSION AX629301

VERSION AX629301.1 GI:28457339

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 6342 11-JUL-2002;

JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers

source 1..11

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 96;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 CCTTCCTAAGC 24
Db 11 CCTTCCTCGGC 1

RESULT 196
AX629429/c

LOCUS AX629429 11 bp DNA linear PAT 21-FEB-2003

DEFINITION Sequence 6470 from Patent WO02053774.

ACCESSION AX629429

VERSION AX629429.1 GI:28457467

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 6470 11-JUL-2002;

JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers

source 1..11

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 96;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CACCTCATCGC 12
Db 11 CGCCTCGTCGC 1

RESULT 197
AX629767/c

LOCUS AX629767 11 bp DNA linear PAT 21-FEB-2003

DEFINITION Sequence 6808 from Patent WO02053774.

ACCESSION AX629767

VERSION AX629767.1 GI:28457805

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6808 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 12 CCCCTTCCTAA 22
1111111111
Db 11 CCCCTCTTAA 1

RESULT 198
AX630305/c
LOCUS AX630305 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7346 from Patent WO02053774.
ACCESSION AX630305
VERSION AX630305.1 GI:28458343
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7346 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ACCTCATCGCC 13
1111111111
Db 11 ACCCATCCCC 1

RESULT 199
AX630373/c
LOCUS AX630373 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7414 from Patent WO02053774.
ACCESSION AX630373
VERSION AX630373.1 GI:28458411
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7414 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CCTCATCGCCC 14
1111111111
Db 11 CCACAGCGCCC 1

RESULT 200
AX630651
LOCUS AX630651 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7692 from Patent WO02053774.
ACCESSION AX630651
VERSION AX630651.1 GI:28458689
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7692 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 TCATCGCCCT 16
1111111111
Db 1 TCAGCGACCT 11

RESULT 201
AX631451
LOCUS AX631451 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8493 from Patent WO02053774.
ACCESSION AX631451
VERSION AX631451.1 GI:28459517
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8493 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 CCCTTCCTAAG 23
1111111111
Db 1 CCTTACCTAAG 11

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RESULT 202
AX631937
LOCUS      AX631937               11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 8979 from Patent WO02053774.
ACCESSION  AX631937
VERSION     AX631937.1   GI:28467552
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)

REFERENCE
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 8979 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source     1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      30.0%;   Score 7.8;   DB 1;   Length 11;
Best Local Similarity 81.8%;   Pred. No. 96;
Matches          9;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      2  CACCTCATCGC 12
        ||||| |||||
Db      1  CACCCCTCGC 11

RESULT 203
AX632012/c
LOCUS      AX632012               11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 9054 from Patent WO02053774.
ACCESSION  AX632012
VERSION     AX632012.1   GI:28467627
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)

REFERENCE
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 9054 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source     1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      30.0%;   Score 7.8;   DB 1;   Length 11;
Best Local Similarity 81.8%;   Pred. No. 96;
Matches          9;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      15 CTTCCCTAAGCA 25
        ||||| |||||
Db      11 CTTCCGCAGCA 1

RESULT 204
AX632294/c
LOCUS      AX632294               11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 9336 from Patent WO02053774.
ACCESSION  AX632294
VERSION     AX632294.1   GI:28467909
KEYWORDS
```

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SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 9336 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      30.0%;   Score 7.8;   DB 1;   Length 11;
Best Local Similarity 81.8%;   Pred. No. 96;
Matches          9;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      8  ATCGCCCTTC 18
        ||| |||||
Db      11 AGCACCTTC 1

RESULT 205
AX632649
LOCUS      AX632649               11 bp    DNA          linear    PAT 21-FEB-2003
DEFINITION Sequence 9691 from Patent WO02053774.
ACCESSION  AX632649
VERSION     AX632649.1   GI:28468264
KEYWORDS
SOURCE
ORGANISM     Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 9691 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      30.0%;   Score 7.8;   DB 1;   Length 11;
Best Local Similarity 81.8%;   Pred. No. 96;
Matches          9;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      12 CCCCTTCCTAA 22
        ||||| |||||
Db      1  CCCCCACCTAA 11

RESULT 206
AX711117
LOCUS      AX711117               11 bp    RNA          linear    PAT 11-APR-2003
DEFINITION Sequence 417 from Patent EP1288296.
ACCESSION  AX711117
VERSION     AX711117.1   GI:29787498
KEYWORDS
SOURCE
ORGANISM     Herpes simplex virus unknown type
            Herpes simplex virus unknown type
            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
            Alphaherpesvirinae; Simplexvirus.
REFERENCE
1
AUTHORS      Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
TITLE        Method and reagent for inhibiting HBV viral replication
JOURNAL      Patent: EP 1288296-A 417 05-MAR-2003;
```


ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kataoka,K.
TITLE Transcriptional activator
JOURNAL Patent: WO 0132860-A 2 10-MAY-2001;
OTSUKA PHARMACEUTICAL CO LTD,KOSUKE KATAOKA
COMMENT OS Artificial Sequence
PN WO 0132860-A/2
PD 10-MAY-2001
PF 15-FEB-2000 WO 2000JP000841
PR 04-NOV-1999 JP 99P 314335
PI KOSUKE KATAOKA
PC C12N15/11,C01G11/00,C01G13/04,C01G7/00,C07C323/52,C07H23/00 CC
Maf recognition element
FH Key Location/Qualifiers.
FEATURES
source 1..13
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 30.0%; Score 7.8; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 CTTCTTAAGCA 25
| | | | |
Db 11 CTTAGTAAGCA 1

RESULT 210
AR124568/c
LOCUS AR124568 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 14 from patent US 6171864.
ACCESSION AR124568
VERSION AR124568.1 GI:14109929
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Coughlan,S.J. and Winfrey,R.J. Jr.
TITLE Calreticulin genes and promoter regions and uses thereof
JOURNAL Patent: US 6171864-A 14 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 29.2%; Score 7.6; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATC 10
: | | : | | | | |
Db 10 YCAVRTCATC 1

RESULT 211
A41385
LOCUS A41385 10 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 11 from Patent WO9426928.
ACCESSION A41385
VERSION A41385.1 GI:2297104
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Strauss,M. and Bauer,D.
TITLE COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL
DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT

JOURNAL Patent: WO 9426928-A 11 24-NOV-1994;
MAX PLANCK GESELLSCHAFT (DE)
COMMENT Other publication DE 4317414 940421.
FEATURES Location/Qualifiers
source 1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 TTCCTAAGC 24
| | | | | | | |
Db 1 TACCTAAGC 9

RESULT 212
A52289
LOCUS A52289 10 bp DNA linear PAT 12-DEC-1997
DEFINITION Sequence 79 from Patent EP0705842.
ACCESSION A52289
VERSION A52289.1 GI:2852024
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Bartnik,E.D. and Margerie,D.D.
TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta
JOURNAL Patent: EP 0705842-A 79 10-APR-1996;
HOECHST AG (DE)
COMMENT Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
FEATURES Location/Qualifiers
source 1..10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 TTCCTAAGC 24
| | | | | | | |
Db 1 TACCTAAGC 9

RESULT 213
AR027855/c
LOCUS AR027855 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 53 from patent US 5856459.
ACCESSION AR027855
VERSION AR027855.1 GI:5938675
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Frank,B.L., Roberts,P.C., Goodchild,J., Craig,J.Charles. and
Mills,J.S.
TITLE Oligonucleotides specific for hepatitis B virus
JOURNAL Patent: US 5856459-A 53 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0; Matches 8; Conservative 0;

QY 9 TCGCCCCCTT 17
Db 10 TCGACCCCTT 2

RESULT 214
AR028295/c
LOCUS AR028295 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5858662.
ACCESSION AR028295
VERSION AR028295.1 GI:5940268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 10)
TITLE Keating,M.T. and Morris,C.A.
JOURNAL Diagnosis of Williams syndrome and Williams syndrome cognitive profile by analysis of the presence or absence of a LIM-kinase gene
FEATURES Patent: US 5858662-A 5 12-JAN-1999;
Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0; Matches 8; Conservative 0;

QY 1 CCACCTCAT 9
Db 9 CAACCTCAT 1

RESULT 215
AR030091
LOCUS AR030091 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 280 from patent US 5861244.
ACCESSION AR030091
VERSION AR030091.1 GI:5943305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 10)
TITLE Wang,C.-G. and Hepburn,A.G.
JOURNAL Genetic sequence assay using DNA triple strand formation
FEATURES Patent: US 5861244-A 280 19-JAN-1999;
Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0; Matches 8; Conservative 0;

QY 12 CCCCTTCTT 20
Db 1 CCCCTTCTT 9

RESULT 216
AR092702/c
LOCUS AR092702 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 14 from patent US 5998193.
ACCESSION AR092702
VERSION AR092702.1 GI:10019454
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 10)
TITLE Keese,P., Stapper,M. and Perriman,R.
JOURNAL Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 14 07-DEC-1999;
Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0; Matches 8; Conservative 0;

QY 9 TCGCCCCCTT 17
Db 9 TCCCCCCTT 1

RESULT 217
AR106686/c
LOCUS AR106686 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 6107078.
ACCESSION AR106686
VERSION AR106686.1 GI:12821216
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 10)
TITLE Keese,P., Stapper,M. and Perriman,R.
JOURNAL Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof
FEATURES Patent: US 6107078-A 14 22-AUG-2000;
Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0; Matches 8; Conservative 0;

QY 9 TCGCCCCCTT 17
Db 9 TCCCCCCTT 1

RESULT 218
BD065077
LOCUS BD065077 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065077
VERSION BD065077.1 GI:22610680
KEYWORDS JP 2001509017-A/13.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE 1 (bases 1 to 10)
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Characterization of the yeast transcriptome
JOURNAL Patent: JP 2001509017-A 13 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/13
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC

Characterization of the yeast transcriptome

FH Key Location/Qualifiers

FT source 1..10

FT /organism='Saccharomyces cerevisiae (yeast)'.

FEATURES

source 1..10

/organism="Saccharomyces cerevisiae"

/mol_type="genomic DNA"

/db_xref="taxon:4932"

Query Match 28.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 ATCGCCCT 16

Db 1 ATCGCCGCT 9

RESULT 219

BD161370/c

LOCUS BD161370 10 bp DNA linear PAT 17-JAN-2003

DEFINITION Human activated Th1 and Th2 cell expression genes.

ACCESSION BD161370

VERSION BD161370.1 GI:27867128

KEYWORDS JP 2002186482-A/192.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 10)

AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.

TITLE Human activated Th1 and Th2 cell expression genes

JOURNAL Patent: JP 2002186482-A 192 02-JUL-2002;

COMMENT OS Homo sapiens (human)

PN JP 2002186482-A/192

PD 02-JUL-2002

PF 19-DEC-2000 JP 2000385816

PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human activated Th1 and Th2 cell expression genes FH Key Location/Qualifiers

FT source 1..10

FT /organism='Homo sapiens (human)'.

FEATURES

source 1..10

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

Query Match 28.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCCCTTCCT 20

Db 10 CCCGTTTCCT 2

RESULT 220

BD166733/c

LOCUS BD166733 10 bp DNA linear PAT 17-JAN-2003

DEFINITION Human liver disease-expressing genes.

ACCESSION BD166733

VERSION BD166733.1 GI:27872545

KEYWORDS JP 2002209591-A/278.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 10)

AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.

Human liver disease-expressing genes

Patent: JP 2002209591-A 278 30-JUL-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002209591-A/278

PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI YAMASHITA

PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,

PC C12P21/08,

PC C12N15/00

CC Human liver disease-expressing genes

FH Key Location/Qualifiers

FT source 1..10

FT /organism='Homo sapiens (human)'.

FEATURES

source 1..10

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match 28.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCCCTTCCT 20

Db 10 CCCGTTTCCT 2

RESULT 221

BD166772/c

LOCUS BD166772 10 bp DNA linear PAT 17-JAN-2003

DEFINITION Human liver disease-expressing genes.

ACCESSION BD166772

VERSION BD166772.1 GI:27872584

KEYWORDS JP 2002209591-A/317.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 10)

AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.

TITLE Human liver disease-expressing genes

JOURNAL Patent: JP 2002209591-A 317 30-JUL-2002;

COMMENT OS Homo sapiens (human)

PN JP 2002209591-A/317

PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI YAMASHITA

PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,

PC C12P21/08,

PC C12N15/00

CC Human liver disease-expressing genes

FH Key Location/Qualifiers

FT source 1..10

FT /organism='Homo sapiens (human)'.

FEATURES

source 1..10

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match 28.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 TCCTAAGCA 25

Db 10 TCCAAAGCA 2

RESULT 222
BD166789/c
LOCUS BD166789 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166789
VERSION BD166789.1 GI:27872601
KEYWORDS JP 2002209591-A/334.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 334 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/334
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 CATCGCCCC 15
Db 10 CATCTCCCC 2
RESULT 223
BD166809
LOCUS BD166809 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166809
VERSION BD166809.1 GI:27872621
KEYWORDS JP 2002209591-A/354.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 354 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/354
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CTCATCGCC 13
Db 1 CCCATCGCC 9
RESULT 224
BD166820
LOCUS BD166820 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166820
VERSION BD166820.1 GI:27872632
KEYWORDS JP 2002209591-A/365.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 365 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/365
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..10
/organism="unidentified"
/mol_type="genomic DNA"
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 ACCTCATCG 11
Db 1 ACATCATCG 9
RESULT 225
BD166995/c
LOCUS BD166995 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166995
VERSION BD166995.1 GI:27872807
KEYWORDS JP 2002209591-A/540.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 540 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)

PN JP 2002209591-A/540
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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/organism='Homo sapiens (human)'.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 17 TCCTAAGCA 25
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Db 10 TCCAAAGCA 2
RESULT 226
BD166996/c
LOCUS BD166996 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166996
VERSION BD166996.1 GI:27872808
KEYWORDS JP 2002209591-A/541.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 541 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/541
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 CATCGCCCC 15
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Db 10 CATCTCCCC 2
RESULT 227
BD225340/c
LOCUS BD225340 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Compositions and methods for the identification of lung tumor cells.
ACCESSION BD225340
VERSION BD225340.1 GI:33035110
KEYWORDS JP 2002509707-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Compositions and methods for the identification of lung tumor cells
JOURNAL Patent: JP 2002509707-A 22 02-APR-2002;
GENZYME CORP
COMMENT OS Artificial Sequence
PN JP 2002509707-A/22
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180
PI 31-MAR-1998 US 60/080037
PC C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
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PC C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
G01N33/566//
PC A61K45/00,A61P9/00,A61P35/00,C12N15/00,C12N5/00 CC
Compositions and methods for the identification of lung tumor cells
FH Key Location/Qualifiers
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CACCTCATC 10
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Db 9 CTCCTCATC 1
RESULT 228
BD238638/c
LOCUS BD238638 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238638
VERSION BD238638.1 GI:33048408
KEYWORDS JP 2002534056-A/56.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 56 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/56
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CTCCTAAG 23
Db |||||||
10 CTCCTAAG 2
RESULT 229
BD238784
LOCUS
DEFINITION
BD238784 Preparation and use of superior vaccines.
ACCESSION
VERSION BD238784.1 GI:33048554
KEYWORDS JP 2002534056-A/202.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 202 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/202
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/089853 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CTCCTAAG 23
Db |||||||
10 CTCCTAAG 2
RESULT 229
BD238784
LOCUS
DEFINITION
BD238784 Preparation and use of superior vaccines.
ACCESSION
VERSION BD238784.1 GI:33048554
KEYWORDS JP 2002534056-A/202.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 202 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/202
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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PC C12N15/00,C12N5/00,C12N15/00
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
Db ||||||
2 CTCCTTCCT 10
RESULT 230
BD238974
LOCUS
DEFINITION
BD238974 Preparation and use of superior vaccines.
ACCESSION
VERSION BD238974.1 GI:33048744
KEYWORDS JP 2002534056-A/392.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 392 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/392
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
Db ||||||
2 CTCCTTCCT 10
RESULT 230
BD238974
LOCUS
DEFINITION
BD238974 Preparation and use of superior vaccines.
ACCESSION
VERSION BD238974.1 GI:33048744
KEYWORDS JP 2002534056-A/392.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 392 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/392
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,

Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0; Matches 8; Conservative

Qy 14 CCTTCCTAA 22
Db 2 CCTTCTAA 10

RESULT 231
BD239042/c

LOCUS BD239042 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD239042

VERSION BD239042.1 GI:33048812

KEYWORDS JP 2002534056-A/460.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10)

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 460 15-OCT-2002;
GENZYME CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/460
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC C12N1/19,
G01N37/00,

CC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

FH Key Location/Qualifiers

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FT /organism='Homo sapiens (human)'. .

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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0; Matches 8; Conservative

Qy 17 TCCTAAGCA 25
Db 10 TCCTAGGCA 2

RESULT 232
BD239478

LOCUS BD239478 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD239478

VERSION BD239478.1 GI:33049248

KEYWORDS JP 2002534056-A/896.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10)

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 896 15-OCT-2002;
GENZYME CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/896
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC C12N1/19,
G01N37/00,

CC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0; Matches 8; Conservative

Qy 3 ACCTCATCG 11
Db 1 ACCCCATCG 9

RESULT 233
BD239549

LOCUS BD239549 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD239549

VERSION BD239549.1 GI:33049319

KEYWORDS JP 2002534056-A/967.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10)

REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 967 15-OCT-2002;

GO1N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CTCATCGCC 13
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Db 10 CTCAACGCC 2
RESULT 236
BD239667
LOCUS BD239667 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239667
VERSION BD239667.1 GI:33049437
KEYWORDS JP 2002534056-A/1085.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1085 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1085
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
GO1N37/00,
PC C12N15/00,C12N5/00,C12N15/00
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QY 11 GCCCCTTCC 19
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Db 1 GCCCCTTGC 9
RESULT 237
BD239766/c
LOCUS BD239766 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239766
VERSION BD239766.1 GI:33049536
KEYWORDS JP 2002534056-A/1184.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1184 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1184
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
GO1N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
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Db 10 CCCGTTCCT 2
RESULT 238
BD240481
LOCUS BD240481 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240481
VERSION BD240481.1 GI:33050251
KEYWORDS JP 2002534056-A/1899.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1899 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1899
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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QY 6 TCATCGCCC 14
Db 1 TCATCTCCC 9
RESULT 239
BD240602/c
LOCUS BD240602 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240602
VERSION BD240602.1 GI:33050372
KEYWORDS JP 2002534056-A/2020.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
TITLE Preparation and use of superior vaccines
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240602
VERSION BD240602.1 GI:33052607
KEYWORDS JP 2002535012-A/27.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 10)
Cheval,L., Elalouf,J.M. and Virlon,B.
Microassay for continuous analysis of gene expression and its
application
Patent: JP 2002535012-A 27 22-OCT-2002;
COMMISSARIAT A L'ENERGIE ATOMIQUE, CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE
OS Artificial Sequence
PN JP 2002535012-A/27
PD 22-OCT-2002
PF 25-JAN-2000 JP 2000596176
PR 27-JAN-1999 EP 99400189.9
PI LYDIE CHEVAL,JEAN MARC ELALOUF,BERANGERE VIRLON PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence:linker
FH Key Location/Qualifiers

JOURNAL Patent: JP 2002534056-A 2020 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/2020
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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/db_xref="taxon:9606"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CCTCATCGC 12
Db 9 CCCCATCGC 1
RESULT 240
BD242837
LOCUS BD242837 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Microassay for continuous analysis of gene expression and its
application.
ACCESSION BD242837
VERSION BD242837.1 GI:33052607
KEYWORDS JP 2002535012-A/27.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 10)
Cheval,L., Elalouf,J.M. and Virlon,B.
Microassay for continuous analysis of gene expression and its
application
Patent: JP 2002535012-A 27 22-OCT-2002;
COMMISSARIAT A L'ENERGIE ATOMIQUE, CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE
OS Artificial Sequence
PN JP 2002535012-A/27
PD 22-OCT-2002
PF 25-JAN-2000 JP 2000596176
PR 27-JAN-1999 EP 99400189.9
PI LYDIE CHEVAL,JEAN MARC ELALOUF,BERANGERE VIRLON PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence:linker
FH Key Location/Qualifiers


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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 GCCCCTTCC 19
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Db      1 GTCCCTTCC 9

RESULT 241
CQ483558/c
LOCUS      CQ483558      10 bp      DNA      linear      PAT 30-JAN-2004
DEFINITION      Sequence 15425 from Patent WO0160860.
ACCESSION      CQ483558
VERSION      CQ483558.1 GI:41449177
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1
AUTHORS      Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE      Genes differentially expressed in human prostate cancer and their
              use
JOURNAL      Patent: WO 0160860-A 15425 23-AUG-2001;
              Millennium Predictive Medicine, Inc. (US)
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 GCCCCTTCC 19
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Db      9 GCCCCTACC 1

RESULT 242
CQ857806
LOCUS      CQ857806      10 bp      DNA      linear      PAT 31-AUG-2004
DEFINITION      Sequence 65 from Patent WO2004070059.
ACCESSION      CQ857806
VERSION      CQ857806.1 GI:51851931
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1
AUTHORS      Figtree,G.A., Farral,M., Channon,K. and Watkins,H.
TITLE      Diagnosis of an estrogen-sensitive disorder
JOURNAL      Patent: WO 2004070059-A 65 19-AUG-2004;
              ISIS INNOVATION LIMITED (GB)
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Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 CCCCTTCCT 20
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Db      9 CCCCTTCT 1

RESULT 244
CS050731
LOCUS      CS050731      10 bp      DNA      linear      PAT 23-MAR-2005
DEFINITION      Sequence 16 from Patent WO2005021755.
ACCESSION      CS050731
VERSION      CS050731.1 GI:61889941
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C.,
              Ermakov,S., Hyldig-Nielsen,J., Schroeder,B., Vatta,P. and Bloch,W.
TITLE      Compositions, methods, and kits for fabricating coded molecular
              tags
JOURNAL      Patent: WO 2005021755-A 16 10-MAR-2005;
              Applera Corporation (US)
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 CCCCTTCCT 20
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Db      9 CCCCTTCT 1

RESULT 244
CS050731
LOCUS      CS050731      10 bp      DNA      linear      PAT 23-MAR-2005
DEFINITION      Sequence 16 from Patent WO2005021755.
ACCESSION      CS050731
VERSION      CS050731.1 GI:61889941
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C.,
              Ermakov,S., Hyldig-Nielsen,J., Schroeder,B., Vatta,P. and Bloch,W.
TITLE      Compositions, methods, and kits for fabricating coded molecular
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JOURNAL      Patent: WO 2005021755-A 16 10-MAR-2005;
              Applera Corporation (US)
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 CCCCTTCCT 20
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 CGCCCTTTC 18
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Db      2 CGCCCTTTC 10

RESULT 243
CS050730/c
LOCUS      CS050730      10 bp      DNA      linear      PAT 23-MAR-2005
DEFINITION      Sequence 15 from Patent WO2005021755.
ACCESSION      CS050730
VERSION      CS050730.1 GI:61889940
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C.,
              Ermakov,S., Hyldig-Nielsen,J., Schroeder,B., Vatta,P. and Bloch,W.
TITLE      Compositions, methods, and kits for fabricating coded molecular
              tags
JOURNAL      Patent: WO 2005021755-A 15 10-MAR-2005;
              Applera Corporation (US)
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 CCCCTTCCT 20
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Db      9 CCCCTTCT 1

RESULT 244
CS050731
LOCUS      CS050731      10 bp      DNA      linear      PAT 23-MAR-2005
DEFINITION      Sequence 16 from Patent WO2005021755.
ACCESSION      CS050731
VERSION      CS050731.1 GI:61889941
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C.,
              Ermakov,S., Hyldig-Nielsen,J., Schroeder,B., Vatta,P. and Bloch,W.
TITLE      Compositions, methods, and kits for fabricating coded molecular
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JOURNAL      Patent: WO 2005021755-A 16 10-MAR-2005;
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 131 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/131
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
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CC
FH Key Location/Qualifiers.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 ACCTCATCG 11
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Db 1 ACATCATCG 9
RESULT 250
AR234531
LOCUS AR234531 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 65 from patent US 6458584.
ACCESSION AR234531
VERSION AR234531.1 GI:27277235
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Mirzabekov,A., Guschin,D.Y., Chik,V., Drobyshev,A., Fotin,A.,
Yershov,G. and Lysov,Y.
TITLE Customized oligonucleotide microchips that convert multiple genetic
information to simple patterns, are portable and reusable
JOURNAL Patent: US 6458584-A 65 01-OCT-2002;
University of Chicago; Chicago, IL
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source 1..10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CACCTCATC 10
| |||||
Db 1 CTCCTCATC 9
RESULT 251
AR236019
LOCUS AR236019 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 16 from patent US 6461871.
ACCESSION AR236019
VERSION AR236019.1 GI:27279404
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kubista,M., Svanvik,N. and Westman,G.
TITLE Method for the preparation of a probe for nucleic acid
hybridization
JOURNAL Patent: US 6461871-A 16 08-OCT-2002;
Lightup Technologies AB; Huddinge;
SEX;
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source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
|| |||||
Db 1 CCTCTTCCT 9
RESULT 252
AR266776
LOCUS AR266776 10 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 139 from patent US 6495336.
ACCESSION AR266776
VERSION AR266776.1 GI:29695849
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ludin,C., Wikstroem,P., Svendsen,L.G. and Schulze,A.
TITLE Oligopeptide derivatives for the electrochemical measurement of
protease activity
JOURNAL Patent: US 6495336-A 139 17-DEC-2002;
Pentapharm AG;;
CHX;
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source Location/Qualifiers
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/mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 18 CCTAAGCAT 26
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Db 2 CCCAAGCAT 10
RESULT 253
AR274332
LOCUS AR274332 10 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 28 from patent US 6506561.
ACCESSION AR274332
VERSION AR274332.1 GI:29706778
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Cheval,L., Elalouf,J.-M. and Virlon,B.
TITLE Method of obtaining a library of tags capable of defining a
specific state of a biological sample
JOURNAL Patent: US 6506561-A 28 14-JAN-2003;
Commissariat a l'Energie Atomique and Centre National de la
Recherche Scientifique-CNRS; Paris;
FRX;
FEATURES
source Location/Qualifiers
1..10


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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
1 (bases 1 to 10)
AUTHORS     Dobrindt,D. and Fischer,U.
TITLE       Device for generating an offset of transported flexible sheet
            material
JOURNAL     Patent: US 6588746-A 1263 08-JUL-2003;
            NexPress Solutions LLC; Rochester, NY;
            DEX;
FEATURES     Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATC 10
      |||||
Db      9 CACCTCCTC 1

RESULT 259
AR351722/c
LOCUS      AR351722      10 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 1264 from patent US 6588746.
ACCESSION  AR351722
VERSION     AR351722.1 GI:33753518
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Dobrindt,D. and Fischer,U.
TITLE      Device for generating an offset of transported flexible sheet
            material
JOURNAL    Patent: US 6588746-A 1264 08-JUL-2003;
            NexPress Solutions LLC; Rochester, NY;
            DEX;
FEATURES   Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATC 10
      |||||
Db      9 CACCTCCTC 1

RESULT 260
AR364130
LOCUS      AR364130      10 bp      DNA      linear      PAT 03-SEP-2003
DEFINITION Sequence 10 from patent US 5256545.
ACCESSION  AR364130
VERSION     AR364130.1 GI:34426456
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Brown,M.S., Goldstein,J.L., Russell,D.W. and Sudhof,T.C.
TITLE      Sterol Regulatory Elements
JOURNAL    Patent: US 5256545-A 10 26-OCT-1993;
            Board of Regents, The University of Texas System; Austin, TX
FEATURES   Location/Qualifiers
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            /organism="unknown"
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/mol_type="genomic DNA"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      18 CCTAAGCAT 26
      |||||
Db      1 CCTATGCAT 9

RESULT 261
AX033052
LOCUS      AX033052      10 bp      DNA      linear      PAT 21-SEP-2000
DEFINITION Sequence 27 from Patent EP1024201.
ACCESSION  AX033052
VERSION     AX033052.1 GI:10279955
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Elalouf,J.M., Cheval,L. and Virlon,B.
TITLE      Microassay for serial analysis of gene expression and applications
            thereof
JOURNAL    Patent: EP 1024201-A 27 02-AUG-2000;
            COMMISSARIAT ENERGIE ATOMIQUE (FR) ; DE CENTRE NAT (FR)
FEATURES   Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="linker"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GCCCCTTCC 19
      |
Db      1 GTCCCTTCC 9

RESULT 262
AX152405/c
LOCUS      AX152405      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 320 from Patent WO0138577.
ACCESSION  AX152405
VERSION     AX152405.1 GI:14534056
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 320 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
      |||
Db      10 CCCGTCCT 2
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RESULT 263
AX152423
LOCUS          AX152423          10 bp      DNA          linear          PAT 22-JUN-2001
DEFINITION     Sequence 338 from Patent WO0138577.
ACCESSION      AX152423
VERSION        AX152423.1  GI:14534074
KEYWORDS
SOURCE
ORGANISM       Homo sapiens (human)
REFERENCE
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 338 31-MAY-2001;
                The Johns Hopkins University (US)
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                /db_xref="taxon:9606"
Query Match    28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY             2 CACCTCATC 10
              ||| |||||
Db             1 CAGCTCATC 9

RESULT 264
AX152557
LOCUS          AX152557          10 bp      DNA          linear          PAT 22-JUN-2001
DEFINITION     Sequence 472 from Patent WO0138577.
ACCESSION      AX152557
VERSION        AX152557.1  GI:14534208
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 472 31-MAY-2001;
                The Johns Hopkins University (US)
FEATURES
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                /organism="Homo sapiens"
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                /db_xref="taxon:9606"
Query Match    28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY             3 ACCTCATCG 11
              ||| |||||
Db             1 ACATCATCG 9

RESULT 265
AX152574
LOCUS          AX152574          10 bp      DNA          linear          PAT 22-JUN-2001
DEFINITION     Sequence 489 from Patent WO0138577.
ACCESSION      AX152574
VERSION        AX152574.1  GI:14534225
KEYWORDS
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SOURCE        Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 489 31-MAY-2001;
                The Johns Hopkins University (US)
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                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match    28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY             11 GCCCCTTCC 19
              ||| |||||
Db             2 GGCCCTTCC 10

RESULT 266
AX152575
LOCUS          AX152575          10 bp      DNA          linear          PAT 22-JUN-2001
DEFINITION     Sequence 490 from Patent WO0138577.
ACCESSION      AX152575
VERSION        AX152575.1  GI:14534226
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 490 31-MAY-2001;
                The Johns Hopkins University (US)
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source         1. .10
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Query Match    28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY             11 GCCCCTTCC 19
              ||| |||||
Db             2 GGCCCTTCC 10

RESULT 267
AX152614/c
LOCUS          AX152614          10 bp      DNA          linear          PAT 22-JUN-2001
DEFINITION     Sequence 529 from Patent WO0138577.
ACCESSION      AX152614
VERSION        AX152614.1  GI:14534265
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE
AUTHORS        Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE          Human transcriptomes
JOURNAL        Patent: WO 0138577-A 529 31-MAY-2001;
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  Query Match      28.5%;   Score 7.4;   DB 1;   Length 10;
  Best Local Similarity 88.9%;   Pred. No. 1e+02;
  Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy      11 GCCCCTTCC 19
      ||||| |||
Db      9 GCCCCCTCC 1

RESULT 268
AX152817/c
LOCUS      AX152817      732 from Patent WO0138577.      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION      Sequence 732 from Patent WO0138577.
ACCESSION      AX152817
VERSION      AX152817.1      GI:14534468
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Homnidae; Homo.
REFERENCE      1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL      Patent: WO 0138577-A 732 31-MAY-2001;
      The Johns Hopkins University (US)
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    /db_xref="taxon:9606"

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  Best Local Similarity 88.9%;   Pred. No. 1e+02;
  Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy      4 CCTCATCGC 12
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Db      9 CCTCGTCGC 1

RESULT 269
AX152828/c
LOCUS      AX152828      743 from Patent WO0138577.      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION      Sequence 743 from Patent WO0138577.
ACCESSION      AX152828
VERSION      AX152828.1      GI:14534479
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Homnidae; Homo.
REFERENCE      1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL      Patent: WO 0138577-A 743 31-MAY-2001;
      The Johns Hopkins University (US)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

  Query Match      28.5%;   Score 7.4;   DB 1;   Length 10;
  Best Local Similarity 88.9%;   Pred. No. 1e+02;
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Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy      17 TCCTAAGCA 25
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Db      10 TCCTAGGCA 2

RESULT 270
AX153307
LOCUS      AX153307      1222 from Patent WO0138577.      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION      Sequence 1222 from Patent WO0138577.
ACCESSION      AX153307
VERSION      AX153307.1      GI:14534958
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Homnidae; Homo.
REFERENCE      1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1222 31-MAY-2001;
      The Johns Hopkins University (US)
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  Best Local Similarity 88.9%;   Pred. No. 1e+02;
  Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy      2 CACCTCATC 10
      ||||| ||
Db      2 CACCTCAGC 10

RESULT 271
AX153579
LOCUS      AX153579      1494 from Patent WO0138577.      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION      Sequence 1494 from Patent WO0138577.
ACCESSION      AX153579
VERSION      AX153579.1      GI:14535230
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Homnidae; Homo.
REFERENCE      1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1494 31-MAY-2001;
      The Johns Hopkins University (US)
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  Query Match      28.5%;   Score 7.4;   DB 1;   Length 10;
  Best Local Similarity 88.9%;   Pred. No. 1e+02;
  Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy      3 ACCTCATCG 11
      || |||||
Db      1 ACATCATCG 9

RESULT 272
AX301337
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LOCUS AX301337 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 51 from Patent WO0185941.
ACCESSION AX301337
VERSION AX301337.1 GI:17382420
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 51 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 ACCTCATCG 11
|||
Db 1 ACATCATCG 9
RESULT 273
AX301502
LOCUS AX301502 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 216 from Patent WO0185941.
ACCESSION AX301502
VERSION AX301502.1 GI:17382585
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 216 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
|||||
Db 1 CCCCTCCCT 9
RESULT 274
AX301503
LOCUS AX301503 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 217 from Patent WO0185941.
ACCESSION AX301503
VERSION AX301503.1 GI:17382586
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
REFERENCE 1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 217 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
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1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
|||||
Db 1 CCCCTCCCT 9
RESULT 275
AX301539
LOCUS AX301539 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 253 from Patent WO0185941.
ACCESSION AX301539
VERSION AX301539.1 GI:17382622
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 253 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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/mol_type="unassigned DNA"
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Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CACCTCATC 10
|||||
Db 2 CACCTCAGC 10
RESULT 276
AX302607/c
LOCUS AX302607 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 125 from Patent WO0175177.
ACCESSION AX302607
VERSION AX302607.1 GI:17383134
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 125 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source
1. .10
/organism="Homo sapiens"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CACCTCATC 10
Db 9 CTCCTCATC 1

RESULT 277
AX377234/c
LOCUS AX377234 10 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 35 from Patent WO0212497.
ACCESSION AX377234
VERSION AX377234.1 GI:19573523
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Choi, J.Y., Kazemi, A. and Koshy, B.
TITLE Haplotypes of the nfkb1b gene
JOURNAL Patent: WO 0212497-A 35 14-FEB-2002;
Genaissance Pharmaceuticals, Inc. (US)
FEATURES
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1. .10
/organism="Homo sapiens"
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Qy 6 TCATCGCCC 14
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RESULT 278
AX465374/c
LOCUS AX465374 10 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 42 from Patent WO0211761.
ACCESSION AX465374
VERSION AX465374.1 GI:21899737
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 42 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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RESULT 279
AX667812/c
LOCUS AX667812 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1261 from Patent WO0242459.
ACCESSION AX667812
VERSION AX667812.1 GI:29291349
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1261 30-MAY-2002;
Sangamo Biosciences Inc. (US)
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Qy 2 CACCTCATC 10
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Db 9 CACCTCCTC 1

RESULT 280
AX667814/c
LOCUS AX667814 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1263 from Patent WO0242459.
ACCESSION AX667814
VERSION AX667814.1 GI:29291351
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1263 30-MAY-2002;
Sangamo Biosciences Inc. (US)
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RESULT 281
AX667815/c
LOCUS AX667815 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1264 from Patent WO0242459.
ACCESSION AX667815
VERSION AX667815.1 GI:29291352

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KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Liu,Q.
TITLE       Position dependent recognition of gnn nucleotide triplets by zinc
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JOURNAL     Patent: WO 0242459-A 1264 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
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QY      2 CACCTCATC 10
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RESULT 282
LOCUS     AX753477/c
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ACCESSION AX753477
VERSION   AX753477.1 GI:32166237
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS    Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE      Composition and methods for the identification of lung tumor cells
JOURNAL    Patent: EP 1310556-A 22 14-MAY-2003;
            GENZYME CORPORATION (US)
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QY      2 CACCTCATC 10
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RESULT 283
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DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007796
VERSION   BD007796.1 GI:18636169
KEYWORDS  JP 2001069993-A/72.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
            1 (bases 1 to 10)
            Matsushima,K., Hashimoto,S. and Suzuki,T.
            LPS activated human monocyte expressing genes
            Patent: JP 2001069993-A 72 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
REFERENCE   1
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE       LPS activated human monocyte expressing genes
JOURNAL     Patent: JP 2001069993-A 72 21-MAR-2001;
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RESULT 284
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DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007887
VERSION   BD007887.1 GI:18636260
KEYWORDS  JP 2001069993-A/163.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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            Matsushima,K., Hashimoto,S. and Suzuki,T.
            LPS activated human monocyte expressing genes
            Patent: JP 2001069993-A 163 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
REFERENCE   1
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE       LPS activated human monocyte expressing genes
JOURNAL     Patent: JP 2001069993-A 163 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
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DEFINITION LPS activated human monocyte expressing genes.
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SOURCE    Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            LPS activated human monocyte expressing genes
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            JAPAN SCIENCE AND TECHNOLOGY CORP
REFERENCE   1
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE       LPS activated human monocyte expressing genes
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DEFINITION LPS activated human monocyte expressing genes.
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SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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            Hominidae; Homo.
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            Matsushima,K., Hashimoto,S. and Suzuki,T.
            LPS activated human monocyte expressing genes
            Patent: JP 2001069993-A 163 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
REFERENCE   1
AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE       LPS activated human monocyte expressing genes
JOURNAL     Patent: JP 2001069993-A 163 21-MAR-2001;
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              PF 28-APR-2000 JP 2000131079
              PR
              PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
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            Matsushima,K., Hashimoto,S. and Suzuki,T.
            LPS activated human monocyte expressing genes
            Patent: JP 2001069993-A 163 21-MAR-2001;
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AUTHORS     Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE       LPS activated human monocyte expressing genes
JOURNAL     Patent: JP 2001069993-A 163 21-MAR-2001;
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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70.356 Million cell updates/sec

Title: US-09-904-968A-4-COPY
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Sequence: 1 ccacctcatgcgccttcctaagcat 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 126 seqs, 1353 residues

Total number of hits satisfying chosen parameters: 252

Minimum DB seq length: 0
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Listing first 127 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 50	7.8	30.0	11	1	US-09-634-262-104	Sequence 104, App
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C 104	7	26.9	10	1	US-08-488-551B-210	Sequence 210, App
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107      7 26.9 10 1 US-08-488-551B-213 Sequence 213, App
c 108      7 26.9 10 1 US-08-488-551B-289 Sequence 289, App
c 109      7 26.9 10 1 US-08-488-551B-290 Sequence 290, App
c 110      7 26.9 10 1 US-08-488-551B-291 Sequence 291, App
c 111      7 26.9 10 1 US-08-488-551B-292 Sequence 292, App
112      7 26.9 10 1 US-08-839-327-12 Sequence 12, Appl
c 113      7 26.9 10 1 US-08-719-337-12 Sequence 12, Appl
114      7 26.9 10 1 US-09-340-781B-12 Sequence 12, Appl
115      7 26.9 10 1 US-08-764-522A-3 Sequence 3, Appli
116      7 26.9 10 1 US-08-764-528-3 Sequence 3, Appli
117      7 26.9 10 1 US-08-872-859-3 Sequence 3, Appli
118      7 26.9 10 1 US-08-522-384-24 Sequence 24, Appl
c 119      7 26.9 10 1 US-09-030-156-27 Sequence 27, Appl
c 120      7 26.9 10 1 US-09-645-757-27 Sequence 27, Appl
c 121      7 26.9 10 1 US-09-229-007A-81 Sequence 81, Appl
c 122      7 26.9 10 1 US-09-508-753B-52 Sequence 52, Appl
c 123      7 26.9 10 1 US-09-508-753B-128 Sequence 128, App
c 124      7 26.9 10 1 US-10-108-280-27 Sequence 27, Appl
c 125      7 26.9 10 1 US-10-113-424-81 Sequence 81, Appl
c 126      7 26.9 10 1 US-09-875-453B-32 Sequence 32, Appl
127      7 26.9 10 1 US-08-956-518A-110 Sequence 110, App
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ALIGNMENTS

```

RESULT 1
US-08-983-605-11
; Sequence 11, Application US/08983605A
; Patent No. 6720137
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticace and the Use of
; TITLE OF INVENTION: Said Markers
; FILE REFERENCE: 2936.10400
; CURRENT APPLICATION NUMBER: US/08/983.605A
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; EARLIER FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-11
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Query Match 49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

Qy 1 CCACCTCATGCCCCCT 16
| |||| |||||
Db 2 CGACCTGATGCCCCCT 17

RESULT 2
US-09-866-108A-242
; Sequence 242, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 242
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-242
```

```

Query Match 46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```

Qy 4 CCTCATCGCCCTTCCT 20
| ||||| |||||
Db 1 CATCCTCGCCCTTCCT 17
```

```

RESULT 3
US-09-866-108A-7555/c
; Sequence 7555, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
```

```

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7555
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7555

Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      9 TCGCCCTTCCTAAGCA 25
Db      17 TGGCCCGTCATAAGCA 1

RESULT 4
US-08-291-932A-33
; Sequence 33, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;

Two
```

```

US-08-291-932A-33

Query Match          41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 20;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTCATCGCC 14
Db      2 CCACCUCACCGGC 15

RESULT 5
US-08-291-932A-126
; Sequence 126, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;

Two

US-08-291-932A-126

Query Match          41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      11 GCCCCTTCCTAAGC 24
Db      1 GUCCCUCCUCAGC 14
```

RESULT 6
US-08-291-932A-153
; Sequence 153, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-291-932A-153

Two

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAAGC 24
| | | | | : | | | | |
Db 1 GUCCCUUCCUCAGC 14

RESULT 7
US-08-291-932A-158
; Sequence 158, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-291-932A-158

Two

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAAGC 24
| | | | | : | | | | |
Db 2 GUCCCUUCCUCAGC 15

RESULT 8
US-08-291-932A-162
; Sequence 162, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California

; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-291-932A-162

Two

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGCCCTTCCT 20
||:| |||:|:
Db 2 CAUGGUCCCUCCU 15

RESULT 9
US-08-363-240A-119
; Sequence 119, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-119

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATGCC 14
||||: :|||
Db 2 CCACCUUCUGGCC 15

RESULT 10
US-08-363-240A-120
; Sequence 120, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 120:


```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-120

Query Match          41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCC 14
Db 1 CCACCUUCUGGCC 14

RESULT 11
US-09-724-857-35/c
; Sequence 35, Application US/09724857
; Patent No. 6855866
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apuya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Polynucleotides Useful for Modulating Transcription
; FILE REFERENCE: 023070-114700US
; CURRENT APPLICATION NUMBER: US/09/724,857
; CURRENT FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:H-AP56 forward
; OTHER INFORMATION: primer
US-09-724-857-35

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CTTTCCTAAGCAT 26
Db 13 CCTTCATAAGCTT 1

RESULT 12
US-09-196-523-49/c
; Sequence 49, Application US/09196523A
; Patent No. 6248525
; GENERAL INFORMATION:
; APPLICANT: Nilsen, Timothy W.
; TITLE OF INVENTION: Method for Identifying and Inactivating Essential or
; TITLE OF INVENTION: Functional Genes
; FILE REFERENCE: ILI 130
; CURRENT APPLICATION NUMBER: US/09/196,523A
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/079,851
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-196-523-49

```

```

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATCGCC 13
Db 12 ACCGCATCGCC 2

RESULT 13
US-10-129-192A-2
; Sequence 2, Application US/10129192A
; Patent No. 6908761
; GENERAL INFORMATION:
; APPLICANT: KATAOKA, Kohsuke
; TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR
; FILE REFERENCE: Q69817
; CURRENT APPLICATION NUMBER: US/10/129,192A
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/JP00/00841
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: JP 1999-314335
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Maf recognition element
US-10-129-192A-2

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTTCTTAAGCA 25
Db 3 CTTACTAAGCA 13

RESULT 14
US-08-467-126-2/c
; Sequence 2, Application US/08467126
; Patent No. 5776744
; GENERAL INFORMATION:
; APPLICANT: GLAZER, PETER M.
; APPLICANT: GEORGE, JAY
; APPLICANT: LIN, L. MICHAEL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: EFFECTING HOMOLOGOUS RECOMBINATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORPHARM, INC.
; STREET: 200 PERRY PARKWAY
; CITY: GAITHERSBURG
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE-3.50 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: APPLE MACINTOSH POWERBOOK 520
; OPERATING SYSTEM: MACINTOSH
; SOFTWARE: WORD PERFECT 3.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,126
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

;
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KARTA, GLENN E.
; REGISTRATION NUMBER: 30,649
; REFERENCE/DOCKET NUMBER: PA-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-527-2058
; TELEFAX: 301-208-6997
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-126-2

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCTTCCT 20
Db 9 CCCCTTCCT 1

RESULT 15
US-08-476-712-1/c
; Sequence 1, Application US/08476712
; Patent No. 5962426
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; TITLE OF INVENTION: Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,712
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-476-712-1

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCTTCCT 20

Db 9 CCCCTTCCT 1
RESULT 16
US-09-411-291-1/c
; Sequence 1, Application US/09411291
; Patent No. 6303376
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; TITLE OF INVENTION: Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411,291
; FILING DATE: 04-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,712
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-411-291-1

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCTTCCT 20
Db 9 CCCCTTCCT 1

RESULT 17
US-08-623-891-31
; Sequence 31, Application US/08623891
; Patent No. 5795778
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles

```

; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,891
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,200
; FILING DATE:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-623-891-31

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCTCATCGCCCC 15
Db 1 CCUCCACGCCCC 12

RESULT 18
US-08-173-489C-262
; Sequence 262, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 262:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from Frankia sp
; DESCRIPTION: 23s region in Seq ID No. 5861244261
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 262 :FROM 1 TO 12
; US-08-173-489C-262

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCTCATCGCCCC 15
Db 1 CCTCTTCCCCC 12

RESULT 19
US-09-340-861-31
; Sequence 31, Application US/09340861
; Patent No. 6432704
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
```

```

;
;   TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 31:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 12
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-09-340-861-31

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 CCTCATCGCCCC 15
      ||:|| |||||
Db      1 CCUCCACGCCCC 12

RESULT 20
US-09-634-262-31.
; Sequence 31, Application US/09634262
; Patent No. 6440719
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/634,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-634-262-31

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 CCTCATCGCCCC 15
      ||:|| |||||
```

```

Db      1 CCUCCACGCCCC 12

RESULT 21
US-08-335-565A-23
; Sequence 23, Application US/08335565A
; Patent No. 5527671
; GENERAL INFORMATION:
; APPLICANT: Li, Kening
; APPLICANT: Rouse, Douglas I.
; APPLICANT: German, Thomas L.
; TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: 1 South Pinckney St., PO BOX 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,565A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.93065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-335-565A-23

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TCATCGCCCC 15
      | |||||
Db      1 TTATCGCCCC 10

RESULT 22
US-08-233-608-44
; Sequence 44, Application US/082333608
; Patent No. 5585238
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,608
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-12
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-233-608-44

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred.No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCC 15
| |||||
Db 1 TTATCGCCCC 10

RESULT 23
US-08-887-480-44
; Sequence 44, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-12
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-887-480-44

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred.No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCC 15
| |||||
Db 1 TTATCGCCCC 10

RESULT 24
US-08-173-489C-223/c
; Sequence 223, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 223:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 23s rRNA gene from Escherichia coli
; DESCRIPTION: (Accession # M25458) nucleotides 1410 to 1419
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; STRAIN: MRE600
; PUBLICATION INFORMATION:
; AUTHORS: Branlant, C, Krol, A, Machatt, M, A,
; AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Koessel,
; AUTHORS: H.
; TITLE: Primary and secondary


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; TITLE: structures of Escherichia coli MRE 600 23S
; TITLE: ribosomal RNA Comparison with models of
; TITLE: secondary structure for maize chloroplast 23S
; TITLE: rRNA and for large portions of mouse and human
; TITLE: 16S mitochondrial rRNAs
; JOURNAL: Nucleic Acids Research
; VOLUME: 9
; PAGES: 4303-4324
; DATE: 1981
; RELEVANT RESIDUES IN SEQ ID NO: 223 :FROM 1 TO 10
US-08-173-489C-223

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```

Query Match      32.3%;      Score 8.4;  DB 1;   Length 10;
Best Local Similarity 90.0%;
Pred. No. 30;
Matches 9;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

QY 9 TCGCCCCCTTC 18
Db 10 TCCCCCCTTC 1

RESULT 25
 US-08-722-187-44
 ; Sequence 44, Application US/08722187
 ; Patent No. 5955274
 ; GENERAL INFORMATION:
 ; APPLICANT: Ligon, James M
 ; APPLICANT: Beck, James J
 ; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
 ; TITLE OF INVENTION: Polymerase Chain Reaction
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ciba-Geigy Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10532
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/722,187

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels

QY 6 TCATCGCCCC 15
| | | | | | | |
Db 1 TTATCGCCCC 10

RESULT 26
US-08-388-353-83/c
; Sequence 83, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-83

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATC 10
|||
Db 10 CCACCCCATC 1

RESULT 27
US-08-388-353-191/c
; Sequence 191, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
;

ADDRESSEE: Scully, Scott, Murphy & Presser

```
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-191

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 CCACCTCATC 10
   ||||| ||
Db 10 CCACCTCTTC 1

RESULT 28
US-08-488-551B-83/c
; Sequence 83, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
```

```
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-83

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 CCACCTCATC 10
   ||||| ||||
Db 10 CCACCCCATC 1

RESULT 29
US-08-488-551B-191/c
; Sequence 191, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
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```
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: DNA
US-08-488-551B-191

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATC 10
Db 10 CCACCTCTTC 1

RESULT 30
PCT-US95-04712-44
; Sequence 44, Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-12
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04712-44

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10

RESULT 31
US-08-173-489C-60
; Sequence 60, Application US/08173489C
```

```
/ ; Patent No. 5861244
/ ; GENERAL INFORMATION:
/ ; APPLICANT: WANG, C. -G.
/ ; APPLICANT: HEPBURN, A. G.
/ ; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
/ ; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
/ ; NUMBER OF SEQUENCES: 365
/ ; CORRESPONDENCE ADDRESS:
/ ; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
/ ; STREET: 510 EAST 73RD STREET,
/ ; CITY: NEW YORK
/ ; STATE: NEW YORK
/ ; COUNTRY: USA
/ ; ZIP: 10021.
/ ; COMPUTER READABLE FORM:
/ ; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
/ ; COMPUTER: IBM PC/XT/AT
/ ; OPERATING SYSTEM: MS-DOS version 6.2
/ ; SOFTWARE: Wordperfect Version 5.1
/ ; CURRENT APPLICATION DATA:
/ ; APPLICATION NUMBER: US/08/173,489C
/ ; FILING DATE: 22 DEC 1993
/ ; CLASSIFICATION: 435
/ ; PRIOR APPLICATION DATA:
/ ; APPLICATION NUMBER: US 07/968,436
/ ; FILING DATE: 29 OCT 1992
/ ; ATTORNEY/AGENT INFORMATION:
/ ; NAME: Handelman, Joseph H.
/ ; REGISTRATION NUMBER: 26,179
/ ; REFERENCE/DOCKET NUMBER: U9518-6
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: (attorney) (212) 708-1880
/ ; TELEFAX: (attorney) (212) 246-8959
/ ; INFORMATION FOR SEQ ID NO: 60:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 11 bases
/ ; TYPE: Nucleic Acid
/ ; STRANDEDNESS: single stranded
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: other nucleic acid
/ ; DESCRIPTION: third strand derived from HER-2
/ ; DESCRIPTION: sequence region in Seq ID No. 586124459
/ ; HYPOTHETICAL: Yes
/ ; ANTI-SENSE: NO
/ ; PUBLICATION INFORMATION:
/ ; RELEVANT RESIDUES IN SEQ ID NO: 60 :FROM 1 TO 11
US-08-173-489C-60

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCGCCCTTC 18
Db 2 TCTCCCTTC 11

RESULT 32
US-09-196-523-16/c
; Sequence 16, Application US/09196523A
; Patent No. 6248525
; GENERAL INFORMATION:
; APPLICANT: Nilsen, Timothy W.
; TITLE OF INVENTION: Method for Identifying and Inactivating Essential or
; TITLE OF INVENTION: Functional Genes
; FILE REFERENCE: ILI 130
; CURRENT APPLICATION NUMBER: US/09/196,523A
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/079,851
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
```

```

; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-196-523-16

Query Match          32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATC 10
    ||||| |||||
Db 11 CCACGTCATC 2

RESULT 33
US-08-441-887A-334/c
; Sequence 334, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 334:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-334
```

```

Query Match          32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 TCCTAAGCAT 26
    ||||| |||||
Db 11 TCCTCAGCAT 2

RESULT 34
US-09-043-149-54/c
; Sequence 54, Application US/090431149
; Patent No. 6355418
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Gunter
; TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the
; TITLE OF INVENTION: Identification of Antisense Binding Sites
; FILE REFERENCE: 020600-272
; CURRENT APPLICATION NUMBER: US/09/043,149
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: PCT/GB96/02275
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: GB 9518864.5
; PRIOR FILING DATE: 1995-09-14
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-043-149-54

Query Match          32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 CCTTCCTAAG 23
    | ||||| |||
Db 10 CTTTCCTAAG 1

RESULT 35
US-09-874-601-134/c
; Sequence 134, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ().()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-134
```

Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTCCTAAGC 24
Db 12 CTCCTAGGC 3

RESULT 36

PCT-US94-08023-3
; Sequence 3, Application PC/TUS9408023
; GENERAL INFORMATION:
; APPLICANT: de Kloet, Siwo R.
; TITLE OF INVENTION: Sex-Specific DNA Probe For Parrots,
; TITLE OF INVENTION: Methods And Kits
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08023
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,198
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: FL20979-34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-08023-3

Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGCA 25
Db 2 TTCCTAACCA 11

RESULT 37

US-08-796-899-16
; Sequence 16, Application US/08796899
; Patent No. 6160202
; GENERAL INFORMATION:
; APPLICANT: BUSTOS, Mauricio M
; APPLICANT: CHERN, Maw-Sheng
; TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
; TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,899
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,544
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 028754-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-796-899-16

Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCA 8
Db 2 CCACCTCA 9

RESULT 38

US-08-796-899-20
; Sequence 20, Application US/08796899
; Patent No. 6160202
; GENERAL INFORMATION:
; APPLICANT: BUSTOS, Mauricio M
; APPLICANT: CHERN, Maw-Sheng
; TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
; TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,899
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,544
; FILING DATE: 07-OCT-1994


```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 028754-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-796-899-20
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACCTCA 8
Db 2 CCACCTCA 9

RESULT 39
US-08-796-899-21
; Sequence 21, Application US/08796899
; Patent No. 6160202
; GENERAL INFORMATION:
; APPLICANT: BUSTOS, Mauricio M
; APPLICANT: CHERN, Maw-Sheng
; TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,899
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,544
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 028754-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-796-899-21
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 CCACCTCA 8
Db 2 CCACCTCA 9

RESULT 40
US-09-534-366A-20/c
; Sequence 20, Application US/09534366A
; Patent No. 6759195
; GENERAL INFORMATION:
; APPLICANT: Bentley, William E.
; APPLICANT: Gill, Ryan T.
; TITLE OF INVENTION: Method of Differential Display of Prokaryotic Messenger
; FILE REFERENCE: Bentley et al., Method of . . .
; CURRENT APPLICATION NUMBER: US/09/534,366A
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PROV 60/126,038
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
US-09-534-366A-20
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TCATCGCC 13
Db 10 TCATCGCC 3

RESULT 41
US-09-442-054A-69
; Sequence 69, Application US/09442054A
; Patent No. 6770738
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Berg, Rolf H.
; APPLICANT: Mollegaard, Neils E.
; TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
; FILE REFERENCE: ISIS4290
; CURRENT APPLICATION NUMBER: US/09/442,054A
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 08/471,907
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/054,363
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/ EP92/01219
; PRIOR FILING DATE: 1992-05-19
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6770738el Sequence
US-09-442-054A-69
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 13 CCCTTCCT 20
Db 1 CCCTTCCT 8

RESULT 42
US-09-941-042C-3
; Sequence 3, Application US/09941042C
; Patent No. 6911541
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark A.
; APPLICANT: Li, Yan
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MOLECULAR DECOYS THAT ALTER PROTEIN
; FILE REFERENCE: 5051-471WO
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 09/941,042C
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-941-042C-3

Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCACCTCA 8
Db 2 CCACCTCA 9

RESULT 43
US-08-196-103A-9
; Sequence 9, Application US/08196103A
; Patent No. 5672472
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Anderson, Kevin
; APPLICANT: Bruice, Thomas A.
; APPLICANT: Davis, Peter
; APPLICANT: Driver, Vickie
; APPLICANT: Hanecak, Ronnie C.
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Wyatt, Jaqueline
; TITLE OF INVENTION: Synthetic Unrandomization of Oligomer
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5672472ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,103A
; FILING DATE: February 22, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 749,000
; FILING DATE: 23-AUG-1991

; ATTORNEY/AGENT INFORMATION:
; NAME: Gaumont, Rebecca R.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-0678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-196-103A-9

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 13 CCCTTCCT 20
Db 1 CCCTTCCT 8

RESULT 44
US-08-357-396-9
; Sequence 9, Application US/08357396
; Patent No. 5698391
; GENERAL INFORMATION:
; APPLICANT: Philip Dan Cook
; APPLICANT: Ecker, David J.
; APPLICANT: Anderson, Kevin
; APPLICANT: Bruice, Thomas A.
; APPLICANT: Davis, Peter
; APPLICANT: Driver, Vickie
; APPLICANT: Freier, Susan, M.
; APPLICANT: Hanecak, Ronnie C.
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Wyatt, Jaqueline
; APPLICANT: Yogesh S. Sanghvi
; TITLE OF INVENTION: Improved Methods for Synthetic Unrandomization
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5698391ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,396
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 749,000
; FILING DATE: 23-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 196,103
; FILING DATE: 22-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439

```

; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: RNA (genomic)
US-08-357-396-9

Query Match          30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCT 20
Db      1 CCCUCCU 8

RESULT 45
US-08-386-141-9
; Sequence 9, Application US/08386141
; Patent No. 5747253
; GENERAL INFORMATION:
;   APPLICANT: Ecker, David J.
;   APPLICANT: Davis, Peter
;   APPLICANT: Vickers, Timothy A.
;   TITLE OF INVENTION: COMBINATORIAL OLIGOMER
;   TITLE OF INVENTION: IMMUNOABSORBANT SCREENING ASSAY FOR TRANSCRIPTION
;   TITLE OF INVENTION: FACTORS AND OTHER BIOMOLECULE BINDING
;   NUMBER OF SEQUENCES: 33
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
;   ADDRESSEE: No. 5747253ris
;   STREET: One Liberty Place - 46th Floor
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: U.S.A.
;   ZIP: 19103
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/386,141
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/032,852
;   FILING DATE: 16 MAR 1993
;   APPLICATION NUMBER: US/07/749,000
;   FILING DATE: 23-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Gaumont, Rebecca R.
;   REGISTRATION NUMBER: 35,152
;   REFERENCE/DOCKET NUMBER: ISIS-0653
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 215-568-3100
;   TELEFAX: 215-568-3439
;   INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: RNA (genomic)
US-08-386-141-9

Query Match          30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCT 20
```

```

Db      1 CCCUCCU 8

RESULT 46
US-08-227-180B-14
; Sequence 14, Application US/08227180B
; Patent No. 5866698
; GENERAL INFORMATION:
;   APPLICANT: Ecker et al.
;   TITLE OF INVENTION: Modulation of Gene Expression
;   TITLE OF INVENTION: Through Interference with RNA Secondary Structure
;   NUMBER OF SEQUENCES: 51
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Jane Massey Licata, Esq.
;   STREET: 210 Lake Drive East, Suite 201
;   CITY: Cherry Hill
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08002
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;   COMPUTER: IBM 486
;   OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
;   SOFTWARE: WORDPERFECT 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/227,180B
;   FILING DATE: April 13, 1994
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/518,929
;   FILING DATE: May 4, 1990
;   APPLICATION NUMBER: PCT/US91/02588
;   FILING DATE: April 15, 1991
;   APPLICATION NUMBER: 07/801,168
;   FILING DATE: No. 5866698ember 20, 1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jane Massey Licata
;   REGISTRATION NUMBER: 32,257
;   REFERENCE/DOCKET NUMBER: ISIS-1420
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (215) 568-3100
;   TELEFAX: (215) 568-3439
;   INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   ANTI-SENSE: yes
US-08-227-180B-14

Query Match          30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCT 20
Db      1 CCCUCCU 8

RESULT 47
US-08-623-891-104
; Sequence 104, Application US/08623891
; Patent No. 5795778
; GENERAL INFORMATION:
;   APPLICANT: Kenneth G. Draper
;   TITLE OF INVENTION: METHOD AND REAGENT FOR
;   TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
;   TITLE OF INVENTION: VIRUS REPLICATION
;   NUMBER OF SEQUENCES: 115
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Lyon & Lyon
```

STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,891
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/238,200
FILING DATE:
APPLICATION NUMBER: US/07/987,133
FILING DATE:
APPLICATION NUMBER: 07/882,921
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-623-891-104

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
| | | | | | | | | | | | | |
Db 1 CCCCCUGCCU 11

RESULT 48
US-08-173-489C-355
Sequence 355, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: p53 gene, nucleotides 1153-1163
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Harlow, E, Williamson, N M, Ralston, R,
AUTHORS: Helfman, D M, Adams T E.
TITLE: Molecular cloning and in
TITLE: vitro expression of a cDNA for human cellular
TITLE: tumor antigen p53
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
PAGES: 1601-1610
DATE: 1985
RELEVANT RESIDUES IN SEQ ID NO: 355 :FROM 1 TO 11
US-08-173-489C-355

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15
| | | | | | | | | | | | | |
Db 1 CTCCTCTCCCC 11

RESULT 49
US-09-340-861-104
Sequence 104, Application US/09340861
Patent No. 6432704
GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/987,133

```

;
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-340-861-104

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CGCCCTTCCT 20
| | | | | : | |
Db 1 CCCCCUGCCU 11

RESULT 50
US-09-634-262-104
; Sequence 104, Application US/09634262
; Patent No. 6440719
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/634,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-634-262-104

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CGCCCTTCCT 20
| | | | | : | |
Db 1 CCCCCUGCCU 11

RESULT 51
US-09-249-155A-240/c
; Sequence 240, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-240

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 CTCCTAAGCA 25
| | | | | | | |
Db 11 CATCATAGCA 1

RESULT 52
5494663-21/c
; Patent No. 5494663
; APPLICANT: YAMADA, MASAAKI;FURUTANI, YASUJI;YAMAYOSHI, MICHIKO;
;NOTAKE, MITSUE;YAMAGISHI, JUNICHI
; TITLE OF INVENTION: TREATMENT OF MICROBIAL INFECTION WITH
; INTERLEUKIN 1 POLYPEPTIDES
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,826
; FILING DATE: 02-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,418
; FILING DATE: 30-SEP-1992
; APPLICATION NUMBER: 496,800
; FILING DATE: 21-MAR-1990
; APPLICATION NUMBER: 812,796
; FILING DATE: 23-DEC-1985
; SEQ ID NO:21:
; LENGTH: 11
5494663-21

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 43;
```

```

;
; LENGTH: 11
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-634-262-104

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CGCCCTTCCT 20
| | | | | : | |
Db 1 CCCCCUGCCU 11

RESULT 51
US-09-249-155A-240/c
; Sequence 240, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-240

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 CTCCTAAGCA 25
| | | | | | | |
Db 11 CATCATAGCA 1

RESULT 52
5494663-21/c
; Patent No. 5494663
; APPLICANT: YAMADA, MASAAKI;FURUTANI, YASUJI;YAMAYOSHI, MICHIKO;
;NOTAKE, MITSUE;YAMAGISHI, JUNICHI
; TITLE OF INVENTION: TREATMENT OF MICROBIAL INFECTION WITH
; INTERLEUKIN 1 POLYPEPTIDES
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,826
; FILING DATE: 02-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,418
; FILING DATE: 30-SEP-1992
; APPLICATION NUMBER: 496,800
; FILING DATE: 21-MAR-1990
; APPLICATION NUMBER: 812,796
; FILING DATE: 23-DEC-1985
; SEQ ID NO:21:
; LENGTH: 11
5494663-21

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 43;
```


Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TCATCGCCCT 16
| | | | | | | | | |
Db 11 TCATCAGCCT 1

RESULT 53
US-10-129-192A-2/c
; Sequence 2, Application US/10129192A
; Patent No. 6908761
; GENERAL INFORMATION:
; APPLICANT: KATAOKA, Kohsuke
; TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR
; FILE REFERENCE: Q69817
; CURRENT APPLICATION NUMBER: US/10/129,192A
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/JP00/00841
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: JP 1999-314335
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Maf recognition element
US-10-129-192A-2

Query Match 30.0%; Score 7.8; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 CTTCTTAAGCA 25
| | | | | | | | | |
Db 11 CTTAGTAAGCA 1

RESULT 54
US-08-675-816-14/c
; Sequence 14, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-675-816-14

Query Match 29.2%; Score 7.6; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATC 10
: | | : | | | |
Db 10 YCAYRTCATC 1

RESULT 55
US-08-468-352-53/c
; Sequence 53, Application US/08468352
; Patent No. 5856459
; GENERAL INFORMATION:
; APPLICANT: Frank, Bruce L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Goodchild, John
; APPLICANT: Craig, J. Charles
; APPLICANT: Mills, John S.
; APPLICANT: Slade, Andrew
; APPLICANT: Roberts, No. 58564591 A.
; APPLICANT: Jupp, Raymond
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR HEPATITIS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,352
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-468-352-53

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCGCCCTT 17
| | | | | | | |
Db 10 TCGACCCTT 2

```
RESULT 56
US-08-678-039A-5/c
; Sequence 5, Application US/08678039A
; Patent No. 5858662
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Morris, Colleen A.
; TITLE OF INVENTION: Diagnosis of Williams Syndrome and
; TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
; TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; STREET: Tower
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,039A
; FILING DATE: 10-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-120A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-678-039A-5

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACCTCAT 9
      | | | | |
Db      9 CAACCTCAT 1

RESULT 57
US-08-173-489C-280
; Sequence 280, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
```

```
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 280:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from C. burnetii
DESCRIPTION: 16s region in Seq ID No. 5861244279
HYPOTHETICAL: yes
ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 280 :FROM 1 TO 10
US-08-173-489C-280

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
      | | | | | | |
Db      1 CCCCTTCCT 9

RESULT 58
US-08-265-484B-14/c
; Sequence 14, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
```

;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-265-484B-14

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCGCCCCCTT 17
|| |||||
Db 9 TCCCCCCTT 1

RESULT 59
US-08-388-353-82/c
; Sequence 82, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-82

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CACCTCATC 10
|||||
Db 10 CACCCCATC 2

RESULT 60
US-08-388-353-84/c
; Sequence 84, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-84

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCAT 9
|||||
Db 9 CCACCCCAT 1

RESULT 61
US-08-388-353-188/c
; Sequence 188, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-388-353-188

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      12 CCCCTTCCT 20
      || |||||
Db      10 CCTCTTCCT 2

RESULT 62
US-08-388-353-189/c
; Sequence 189, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
```

```
;
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-189

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      12 CCCCTTCCT 20
      || |||||
Db      9 CCTCTTCCT 1

RESULT 63
US-08-388-353-190/c
; Sequence 190, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-190

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      2 CACCTCATC 10
```

```
Db          10 CACCTCTTC 2
|||||
RESULT 64
US-08-388-353-192/c
; Sequence 192, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-192

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          1 CCACCTCAT 9
|||||
Db          9 CCACCTCTT 1

RESULT 65
US-08-388-353-280/c
; Sequence 280, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
```

```
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 280:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-280

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TCGCCCTT 17
|||||
Db          10 TCCCCCTT 2

RESULT 66
US-08-388-353-281/c
; Sequence 281, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
```


TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-281

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCCCT 17
||| |||||
Db 9 TCCCCCCTT 1

RESULT 67
US-08-488-551B-82/c
; Sequence 82, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-82

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CACCTCATC 10
||||| |||
Db 10 CACCCCATC 2

RESULT 68
US-08-488-551B-84/c
; Sequence 84, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-84

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCAT 9
||||| |||
Db 9 CCACCCCAT 1

RESULT 69
US-08-488-551B-188/c
; Sequence 188, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon

```
;
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-188

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      12 CCCCTTCCT 20
Db      10 CCTCTTCCT 2

RESULT 70
US-08-488-551B-189/c
; Sequence 189, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-189

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      12 CCCCTTCCT 20
Db      9 CCTCTTCCT 1

RESULT 71
US-08-488-551B-190/c
; Sequence 190, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
```

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; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-190

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      2 CACCTCATC 10
      |||||
Db      10 CACCTCTTC 2

RESULT 72
US-08-488-551B-192/c
; Sequence 192, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-192

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      1 CCACCTCAT 9
      |||||
Db      9 CCACCTCTT 1

RESULT 73
US-08-488-551B-280/c
; Sequence 280, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 280:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-280

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

Qy      9 TCGCCCTT 17
      |||||
Db      10 TCCCCCTT 2
```

RESULT 74
US-08-488-551B-281/c
; Sequence 281, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-281

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTT 17
|| |||||
Db 9 TCCCCCTT 1

RESULT 75
US-08-765-257A-14/c
; Sequence 14, Application US/08765257A
; Patent No. 6107078
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes
; TITLE OF INVENTION: and Compositions Thereof

; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH, 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,257A
; FILING DATE: June 24, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 977 9550
; TELEFAX: 212 977 9809
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-765-257A-14

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTT 17
|| |||||
Db 9 TCCCCCTT 1

RESULT 76
US-09-261-115-65
; Sequence 65, Application US/09261115
; Patent No. 6458584
; GENERAL INFORMATION:
; APPLICANT: MIRZABEKOV, ANDREI
; APPLICANT: GUSCHIN, DMITRY Y.
; APPLICANT: SHIK, VALENTINE
; APPLICANT: DROBYSHEV, ALEKSEI
; APPLICANT: FOTIN, ALEXANDER
; APPLICANT: YERSHOV, GENNADIY
; APPLICANT: LYSOV, YU
; TITLE OF INVENTION: CUSTOMIZED OLIGONUCLEOTIDE MICROCHIPS THAT CONVERT
; TITLE OF INVENTION: MULTIPLE GENETIC INFORMATION TO SIMPLE PATTERNS, ARE
; TITLE OF INVENTION: PORTABLE AND REUSABLE
; FILE REFERENCE: 21416/90184
; CURRENT APPLICATION NUMBER: US/09/261,115
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Customized
; OTHER INFORMATION: oligonucleotide
US-09-261-115-65

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;

```
Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      2  CACCTCATC 10
      | | | | | | | |
Db      1  CTCCTCATC 9

RESULT 77
US-09-486-853-16
; Sequence 16, Application US/09486853
; Patent No. 6461871
; GENERAL INFORMATION:
; APPLICANT: KUBISTA, MIKAEL
; APPLICANT: SVANVIK, NICKE
; APPLICANT: WESTMAN, GUNNAR
; TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROBE FOR NUCLEIC ACID HYBRIDIZATION
; FILE REFERENCE: GOTEPO29US
; CURRENT APPLICATION NUMBER: US/09/486,853
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/SE98/01580
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: SE 9703251-0
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-486-853-16

      Query Match      28.5%;  Score 7.4;  DB 1;  Length 10;
      Best Local Similarity 88.9%;  Pred. No. 45;
      Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      12  CCCCTTCCT 20
      | | | | | | | |
Db      1  CCTCTTCCT 9

RESULT 78
US-09-914-259-139
; Sequence 139, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
; OTHER INFORMATION: elements
US-09-914-259-139

      Query Match      28.5%;  Score 7.4;  DB 1;  Length 10;
      Best Local Similarity 88.9%;  Pred. No. 45;
      Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      18  CCTAAGCAT 26
      | | | | | | | |
Db      2  CCCAAGCAT 10

RESULT 79
```

```
US-09-301-721A-28
; Sequence 28, Application US/09301721A
; Patent No. 6506561
; GENERAL INFORMATION:
; APPLICANT: CHEVAL, Lydie
; APPLICANT: ELALOUP, Jean-Marc
; APPLICANT: VIRLON, Berangere
; TITLE OF INVENTION: MICROASSAY FOR SERIAL ANALYSIS OF GENE EXPRESSION AND
; FILE REFERENCE: 0846-0499-0X
; CURRENT APPLICATION NUMBER: US/09/301,721A
; CURRENT FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EPO 99400189.9
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA
US-09-301-721A-28

      Query Match      28.5%;  Score 7.4;  DB 1;  Length 10;
      Best Local Similarity 88.9%;  Pred. No. 45;
      Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      11  GCCCCTTCC 19
      | | | | | | | |
Db      1  GTCCTTCC 9

RESULT 80
US-09-508-753B-423
; Sequence 423, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 423
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-423

      Query Match      28.5%;  Score 7.4;  DB 1;  Length 10;
      Best Local Similarity 88.9%;  Pred. No. 45;
      Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      16  TTCCTAAGC 24
      | | | | | | | |
Db      1  TACCTAAGC 9

RESULT 81
US-09-508-753B-457
; Sequence 457, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
```



```
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 457
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-457
```

```
Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      16 TTCCTAAGC 24
      ||| |||||
Db       2 TTCGTAAGC 10
```

```
RESULT 82
US-09-508-753B-464/c
; Sequence 464, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 464
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-464
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```
Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      16 TTCCTAAGC 24
      ||| |||||
Db       9 TTCGTAAGC 1
```

```
RESULT 83
US-09-721-777-10/c
; Sequence 10, Application US/09721777
; Patent No. PP13279
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Kumar, Sushil
; APPLICANT: Shasany, Ajit Kumar
```

```
; APPLICANT: Dhawan, Sunita
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Dhawan, Om Parkash
; APPLICANT: Singh, Anil Kumar
; APPLICANT: Patra, Nirmal Kumar
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ram Prakash
; TITLE OF INVENTION: Mint Plant Named Saksham
; FILE REFERENCE: 033166-002
; CURRENT APPLICATION NUMBER: US/09/721,777
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPT primer
US-09-721-777-10
```

```
Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      15 CTTCTTAAG 23
      ||||| |||
Db       10 CTTCCGAAG 2
```

```
RESULT 84
5256545-10
; Patent No. 5256545
; APPLICANT: BROWN, MICHAEL S.;GOLDSTEIN, JOSEPH L.;RUSSELL,
; DAVID W.;SUDHOF, THOMAS C.
; TITLE OF INVENTION: STEROL REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/425,852
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 33,330
; FILING DATE: 30-MAR-1987
; APPLICATION NUMBER: 33,081
; FILING DATE: 30-MAR-1987
; SEQ ID NO:10:
; LENGTH: 10
5256545-10
```

```
Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      18 CCTAAGCAT 26
      ||||| ||||
Db       1 CCTATGCAT 9
```

```
RESULT 85
US-08-250-310-12
; Sequence 12, Application US/08250310
; Patent No. 5559005
; GENERAL INFORMATION:
; APPLICANT: Conder, Michael J.
; APPLICANT: McAda, Phyllis
; APPLICANT: Rambosek, John
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: No. 5559005el Bioprocess for Preparing 7-ACA and 7-ADAC
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Ave
```

;
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,310
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/953,492
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Speer, Raymond M.
; REGISTRATION NUMBER: 26,810
; REFERENCE/DOCKET NUMBER: 18572IA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4481
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-250-310-12

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTCCTCA 21
|||||
Db 3 CTCCTCA 9

RESULT 86
US-08-439-404-12
; Sequence 12, Application US/08439404
; Patent No. 5629171
; GENERAL INFORMATION:
; APPLICANT: Conder, Michael J.
; APPLICANT: McAda, Phyllis
; APPLICANT: Rambosek, John
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: No. 5629171el Bioprocess for Preparing 7-ACA and 7-ADAC
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen, III
; STREET: 126 E. Lincoln Ave; P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,404
; FILING DATE: 11-May-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 18572DA
; TELECOMMUNICATION INFORMATION:

;
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-439-404-12

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTCCTCA 21
|||||
Db 3 CTCCTCA 9

RESULT 87
US-08-507-598-3
; Sequence 3, Application US/08507598
; Patent No. 5834188
; GENERAL INFORMATION:
; APPLICANT: HARADA, SHUN-ICHI
; APPLICANT: SAMPATH, T. K.
; APPLICANT: RODAN, GIDEON A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,598
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "AP1 MUTATION"
; US-08-507-598-3

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCATC 10

Db
|||||
3 CCTCATC 9

RESULT 88
US-08-173-489C-303/c
; Sequence 303, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 303:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 16S rRNA gene from Chlamydia psittaci
; DESCRIPTION: (Accession # M13769) nucleotides 1181 to 1190
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Chlamydia psittaci
; PUBLICATION INFORMATION:
; AUTHORS: Weisburg, W G, Hatch, T P, Woese, C R.
; TITLE: Eubacterial Origin of
; TITLE: Chlamydiae
; JOURNAL: Journal of Bacteriology
; VOLUME: 167
; PAGES: 570-574
; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 303 :FROM 1 TO 10
US-08-173-489C-303

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCTTCCT 20
|||||
Db 10 CCTTCCT 4

RESULT 89
US-08-545-253A-12/c
; Sequence 12, Application US/08545253A
; Patent No. 5908978
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; APPLICANT: Henry V. Amerson
; APPLICANT: Phillip Wilcox
; APPLICANT: E. George Kuhlman
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
; TITLE OF INVENTION: SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5908978th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,253A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-545-253A-12

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CCTAAGC 24
|||||
Db 10 CCTAAGC 4

RESULT 90
US-08-507-750-3
; Sequence 3, Application US/08507750
; Patent No. 5932716
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, T. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA

;
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,750
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "APl MUTATION"
US-08-507-750-3

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCTCATC 10
|||||||
Db 3 CCTCATC 9

RESULT 91

US-08-905-567-1
; Sequence 1, Application US/08905567
; Patent No. 6004750
; GENERAL INFORMATION:
; APPLICANT: Frank-Kamenetskii, Maxim D.
; APPLICANT: Veselkov, Alexei G.
; APPLICANT: Demidov, Vadim V.
; TITLE OF INVENTION: Nucleic Acid Clamps
; FILE REFERENCE: BU-03172
; CURRENT APPLICATION NUMBER: US/08/905,567
; CURRENT FILING DATE: 1997-08-04
; EARLIER APPLICATION NUMBER: 08/546,346
; EARLIER FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-905-567-1

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCTTC 18
|||||||
Db 2 CCCCTTC 8

RESULT 92

US-08-388-353-193/c
; Sequence 193, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-193

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACCTC 7
|||||||
Db 8 CCACCTC 2

RESULT 93

US-08-388-353-194/c
; Sequence 194, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-194
```

```
Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 CCACCTC 7
        |||||||
Db       7 CCACCTC 1
```

```
RESULT 94
US-08-388-353-210
; Sequence 210, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-210
```

```
Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CACCTCA 8
        |||||||
Db       4 CACCTCA 10
```

```
RESULT 95
US-08-388-353-211
; Sequence 211, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-211
```

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Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      2 CACCTCA 8
        |||||||
Db       3 CACCTCA 9
```

```
RESULT 96
US-08-388-353-212
; Sequence 212, Application US/08388353
; Patent No. 6010895
```


;
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-212

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCTCA 8
| | | | |
Db 2 CACCTCA 8

RESULT 97
US-08-388-353-213
; Sequence 213, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-213

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCTCA 8
| | | | |
Db 1 CACCTCA 7

RESULT 98
US-08-388-353-289/c
; Sequence 289, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 289:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
US-08-388-353-289

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCC 19
Db      10 CCCTTCC 4

RESULT 99
US-08-388-353-290/c
; Sequence 290, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 290:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-291

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCC 19
Db      8 CCCTTCC 2

RESULT 101
US-08-388-353-292/c
; Sequence 292, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
```

```
;
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 292:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-292

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 CCCTTCC 19
Db      7 CCCTTCC 1

RESULT 102
US-08-488-551B-193/c
; Sequence 193, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-193

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACCTC 7
Db      8 CCACCTC 2

RESULT 103
US-08-488-551B-194/c
; Sequence 194, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-194

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACCTC 7
Db      7 CCACCTC 1
```

```
RESULT 104
US-08-488-551B-210
; Sequence 210, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-210

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
Db 4 CACCTCA 10

RESULT 105
US-08-488-551B-211
; Sequence 211, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-211

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
Db 3 CACCTCA 9

RESULT 106
US-08-488-551B-212
; Sequence 212, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
```

;
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-212

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
|||
Db 2 CACCTCA 8

RESULT 107
US-08-488-551B-213
; Sequence 213, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-213

;
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-213

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
|||
Db 1 CACCTCA 7

RESULT 108
US-08-488-551B-289/c
; Sequence 289, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 289:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-289

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCC 19
Db 10 CCCTTCC 4

RESULT 109

US-08-488-551B-290/c
; Sequence 290, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 290:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-290

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCC 19
Db 9 CCCTTCC 3

RESULT 110

US-08-488-551B-291/c
; Sequence 291, Application US/08488551B

; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 291:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-291

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCC 19
Db 8 CCCTTCC 2

RESULT 111

US-08-488-551B-292/c
; Sequence 292, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.

ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-292

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCC 19
Db 7 CCCTTCC 1

RESULT 112
US-08-839-327-12
Sequence 12, Application US/08839327
Patent No. 6017726
GENERAL INFORMATION:
APPLICANT: CONDER, MICHAEL;
APPLICANT: MCADA, PHYLLIS; RAMBOSEK, JOHN;
APPLICANT: REEVES, CHRISTOPHER
TITLE OF INVENTION: NOVEL BIOPROCESS FOR
TITLE OF INVENTION: PREPARING 7-ACA AND 7-ADAC
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN, MUSERLIAN AND
ADDRESSEE: LUCAS, LLP
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,327
FILING DATE: 17-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 439,404

FILING DATE: 11-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 250,310
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 953,492
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 777,833
FILING DATE: 15-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 253.171-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-839-327-12

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTCCCTA 21
Db 3 CTTCCCTA 9

RESULT 113
US-08-719-337-12/c
Sequence 12, Application US/08719337
Patent No. 6054634
GENERAL INFORMATION:
APPLICANT: O'Malley, David M.
APPLICANT: Sederoff, Ronald R.
APPLICANT: Grattapaglia, Dario
TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN
TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 6054634th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,337
FILING DATE: 25-SEP-1996
CLASSIFICATION: 047
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,567
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102

;
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,528
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-127
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "AP1 SEQUENCE A MUTATION"
;
US-08-764-528-3

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCTCATC 10
| | | | |
Db 3 CCTCATC 9

RESULT 117
US-08-872-859-3
; Sequence 3, Application US/08872859
; Patent No. 6110460
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, T. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,859
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/507,750
; FILING DATE: 26-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100

;
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "AP1 MUTATION"
;
US-08-872-859-3

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCTCATC 10
| | | | |
Db 3 CCTCATC 9

RESULT 118
US-08-522-384-24
; Sequence 24, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
;
US-08-522-384-24

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCTCATC 10
| | | | |
Db 1 CCTCATC 7

RESULT 119
US-09-030-156-27/c
; Sequence 27, Application US/09030156
; Patent No. 6207373
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; TITLE OF INVENTION: POLYMORPHISMS IN DNA
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 221/157
; CURRENT APPLICATION NUMBER: US/09/030,156
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-030-156-27

Query Match 26.9%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTCCCTA 21
|||||||
Db 10 CTTCCCTA 4

RESULT 120

US-09-645-757-27/c
; Sequence 27, Application US/09645757
; Patent No. 6395493
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229
; CURRENT APPLICATION NUMBER: US/09/645,757
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-645-757-27

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTCCCTA 21
|||||||
Db 10 CTTCCCTA 4

RESULT 121

US-09-229-007A-81/c
; Sequence 81, Application US/09229007A
; Patent No. 6453242
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselected Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/09/229,007A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: soybean FAD2-1 cDNA target segment FAD 4
US-09-229-007A-81

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACCTC 7
|||||||
Db 7 CCACCTC 1

RESULT 122

US-09-508-753B-52/c
; Sequence 52, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 52
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-52

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCTCA 8
|||||||
Db 7 CACCTCA 1

RESULT 123

US-09-508-753B-128/c
; Sequence 128, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 128
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-128

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GCCCCTT 17
|||||||
Db 10 GCCCCTT 4

RESULT 124

US-10-108-280-27/c
; Sequence 27, Application US/10108280
; Patent No. 6753148


```
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; TITLE OF INVENTION: POLYMORPHISMS IN DNA
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229
; CURRENT APPLICATION NUMBER: US/10/108,280
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US/09/645,757
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-280-27

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15 CTTCTTA 21
Db      10 CTTCTTA 4

RESULT 125
US-10-113-424-81/c
; Sequence 81, Application US/10113424
; Patent No. 6785613
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselected Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/10/113,424
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US/09/229,007A
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: soybean FAD2-1 cDNA target segment FAD 4
US-10-113-424-81

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACCTC 7
Db      7 CCACCTC 1

RESULT 126
US-09-875-453B-32/c
; Sequence 32, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
```

```
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Vancomycin resistant enterococcus
US-09-875-453B-32

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 TTCCTAA 22
Db      7 TTCCTAA 1

RESULT 127
US-08-956-518A-110
; Sequence 110, Application US/08956518A
; Patent No. 6875606
; GENERAL INFORMATION:
; APPLICANT: Leonard, Sherry
; APPLICANT: Freedman, Robert
; TITLE OF INVENTION: ALPHA-7 NICOTINIC RECEPTOR
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,518A
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-03042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-705-8410
; TELEFAX: 415-397-8338
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-956-518A-110
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Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 TAAGCAT 26
|||
Db 2 TAAGCAT 8

Search completed: May 9, 2006, 16:54:32
Job time : 0.001 secs

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